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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on:

May 9, 2006, 16:57:17 ; Search time 0.001 Seconds (without alignments) 446.576 Million cell updates/sec

US-09-904-968A-4-COPY 26 Title: Perfect score:

1 ccacctcatcgccccttcctaagcat 26 Sequence:

Scoring table:

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Total number of hits satisfying chosen parameters: 729 segs, 8588 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 729 summaries ngsdb4:*

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The present invention relates to compositions and methods useful for the identification and detection of polycystic kidney disease (PKD1) gene mutations. The invention also relates to primers comprising a 5' region having a sequence that selectively hybridises to a PKD1 gene sequence and optionally, to a PKD1 homologue sequence and an adjacent 3' region having a sequence that selectively hybridises to a PKD1 gene sequence and not to a PKD1 homologue sequence. Primer pairs of the invention are useful for a electing the presence or absence of a mutation in a PKD1 polynucleotide in a sample, for identifying a subject at risk for a PKD1-associated disorder such as autosomal dominant polycystic kidney disease (ADPKD) or a subject. They are useful for selectively amplifying a region of a PKD1 can be pKD1 polynucleotide in a sample, as a probe for an amplifying a region of a PKD1 can be pKD1 polynucleotide in a sample, as a probe for an amplification containing the presence of a mutant pKD1 polynucleotide in a sample, as a probe for an amplification containing the presence of a mutant cannal sequence is a PKD1 expression and for engineering transgenic animals. The present sequence is a PKD primer used to generate human PKD1 can an and problems and probl
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                          Novel primer for diagnosing polycystic kidney disease-associated disorder, comprises regions having sequence that selectively hybridizes to polycystic kidney disease gene sequence.
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bin 6.02-6.04; bin 10.04-10.06; bin 1.03-1.06; bin 1.03-1.11;
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chromosome 15; SSR marker; marker assisted breedding; PCR; primer; ss.
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                                                                                                                                  Claim 6; Page 98; 192pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of producing a transformable corn line

CC by introgressing at least one chromosomal locus mapping to bin 6.02-6.04

or bin 10.04-10.06, where the locus is introgressed from a more

Cransformable corn line into a less transformable corn line. The

invention also relates to corn variety 178-187-20 seed (ATCC accession

CC no. PTA-5183) and corn variety 178-187-20 seed (ATCC accession

CC progeny comprises loci mapping to chromosomal bins 1.03-1.06, 1.08-1.11,

CC 3.05-3.07, and 6.02-6.04; a transgenic corn plant produced by

CC ansforming the progeny cited above; and hybrid corn seed and plants

CC ransforming the progeny cited above; and hybrid corn seed and plants

CC produced by crossing a corn line with the progeny cited above. Bacause

CC more transformable lines are trypically agronomically poor, while lines

CC with superior or desired agronomic traits tend to be less transformable,

CC fan introduced gene on traits such as yield, kernel quality and plant

CC fan introduced gene on traits such as yield, kernel quality and plant

CD ADN61671-ADN61702 represent PCR primers used in an example of the

CC invention to amplify corn SSR markers useful in marker assisted breeding.
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microsatellite marker; hypervariable genomic fragment; Triticum aestivum; wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplify; polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum (wheat) or the tribe Triticeae, consist of a sequence tagged site (STS), defined by 2 specific primers (of mean size 17-23 bases) that flank a microsatellite sequence at both ends, which can be amplified to polymorphisms (PCR products of different sizes). The microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primers for STS micro:satellite markers for wheat and related species useful for genetic mapping, analysis and labelling etc. of wheat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite markers based on hypervariable genomic fragments, from
                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                           55.4%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                               Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Example 3; SEQ ID NO 6; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 6; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                  6 TCATCGCCCCTTCCTA 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95DE-01025284
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.8%,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plaschke J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-053731/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE19525284-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roeder M,
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Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; anotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; inizyme; lymphoma; leukaemia; human immunodeficiency virus; HIV associated NHL; lymphoma; leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA, Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkinson's disease; ataxia; Huntington's disease;
tetra-nucleotide sequences, combination microsatellite sequences or an
                    imperfect sequence in which individual bases are mutated. The microsatellite markers can be used for genetic analysis of hexaploid and incrosatellite markers can be used for genetic analysis of hexaploid and microsatellite markers of wheat and for genetic mapping or labelling of monogenic and polygenic properties, and for their selection; for analysing relationships and identifying varieties and for evaluating analysing relationships and identification and plant growth. The markers can differentiate between almost all European wheat lines and show a higher degree of DNA polymorphism than known probes for the wheat genome. They can be detected by PCR, so large numbers of samples can be analysed easily (e.g. several hundred per day). Microsatellite marker-related polymorphisms are stably inherited so can also serve as genetic markers. AAT77003-22 and AAT77535-716 are primer pairs that define the markers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 3 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOGO Amberzyme #219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCSWIGGEN J.
CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-607195/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200159103-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK02547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIBO-)
(BLAT/)
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ABK02547/c
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (MOZO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids an NCH motif), a G-cleaver (cleaving RNA with a NYM motif) propersessing an NCH motif), a G-cleaver (cleaving RNA with an NCH motif), a dicaborate cation that is preferably MG<sup>2</sup>+.

CD DOI in the presence of a divalent cation that is preferably MG<sup>2</sup>+.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-theorytopaemia, and inflammatory arthropathy. The NOGO-targetting nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Eurthermore, the cargetting nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the cargetting nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the contacted may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of the treatment may further comprise the use of one or more content central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), heartingon's disease, muscular dystrophy, and/or other neurodegenerative disease teates which respond to the modulation of NGGO expression. The present secuence is an amberzyme molecule of the invention.
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growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.9%; Score 12.2; DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is an amberzyme molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 17 BP; 6 A; 2 C; 6 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 56;
0; Mismatches
                                                                      Claim 88; Page 135; 200pp; English
                          central nervous system injury.
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2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 82.4%;
les 14; Conservative
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21-SEP-2000; 2
27-SEP-2000; 2
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ID ABN0
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 protein substrates, to hGDMLP-1 protein substrates, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule acopture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The collaborated sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                               New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
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                                                                                                                                                                                                                                                                                                      Shannon ME;
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                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 1 A; 11 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 242; 214pp; English.
                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                          2001WO-US000664
                                                                                                                    2001WO-US000666.
2001WO-US000667.
                                                                                                                                                           2001WO-US000668.
2001WO-US000669.
                                     2001WO-US000662
2001WO-US000663
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                                                                                                                                                                                                                                                                                                    Ji Y, Penn SG,
                                                                                                                                                                                                                                                               (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-179446/23.
                                                                          30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                         30-JAN-2001;
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                                     30-JAN-2001;
                                                                                                                                      30-JAN-2001;
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                                                                                                                                                                                                                                                                                                    Gu Y,
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(first entry)

02-DEC-2004

ACN70653;

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 uncleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to protein variants having desired phenotypic improvements, and for protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specific ally of hGDMLP-1 proteins, as specific ally of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 proteins, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1 in particular heart may be and shelt all muscle disorders. hGDMLP-1 is localised to chromosome 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide, for raising antibodies that recognize hGDWLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDWLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an oligomer used in the screening of the hGDWLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 7555; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                              2001WO-US000661.
2001WO-US000662.
2001WO-US000663.
2001WO-US000664.
2001WO-US000665.
                                                                                                                                                   2000US-0207456P.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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2001WO-US000667.
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                                                                                                                 25-MAY-2001; 2001WO-US016981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AEOM-) AEOMICA INC.
                                      WO200192524-A2.
                                                                                                                                                                                                                                                                     30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
  Homo sapiens.
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04-OCT-2000;
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                                                                          06-DEC-2001
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/ Match 46.9%; Score 12.2; DB 1; Length 17; Local Similarity 82.4%; Pred. No. 56; nes 14; Conservative 0; Mismatches 3; Indels
     Query Match
                            Best Loc
Matches
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Gaps

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9 TCGCCCCTTCCTAAGCA 25 17 TGGCCCCGTCATAAGCA

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ACN70653 standard; DNA; 17 BP
ACN70653/c
ID ACN706
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RESULT 7

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Gape

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Query Match 46.9%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 56; Matches 14; Conservative 0; Mismatches 3; Indels

The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and 55% identity to (S1). A polypeptide of the invention acts as a agonist or pharmaceutical composition of the inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of phermaceutical composition of the invention is useful function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103 Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle Human; 88; probe; myosin-like protein-1; hGDMLP-1; hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder; skeletal muscle function. Shannon ME; Chen W, Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other; Hanzel DK, Rank D, Disclosure; SEQ ID NO 7555; Opp; English. Human GDMLP-1 probe SEQ ID NO:7555. 2001WO-US000664. 2001WO-US000665. 2001WO-US000667. 2001WO-US000669. 2001WO-US000669. 2000GB-00024263. 2001WO-US000661. 2001WO-US000662. 26-NOV-2003; 2003US-00723361 2000US-0234687P 2000US-0236359P 2001WO-US000663 25-MAY-2001; 2001US-00866108 Ji Y, Penn SG, PENN S G. HANZEL D K. RANK D. CHEN W. WPI; 2004-533378/51. US2004137589-A1. 04-OCT-2000; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; Homo sapiens. 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 21-SEP-2000; 27-SEP-2000; 15-JUL-2004. function. (RANK/) I (CHEN/) ((SHAN/) S (JIYY/) (PENN/) (GUXX/) (HANZ/) Gu Y,

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Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                Human; 88; probe; myosin-like protein-1; hGDWLP-1;
hGDWLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shannon ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                 Human GDMLP-1 probe SEQ ID NO:242.
TCGCCCCTTCCTAAGCA 25
                                                             ACN63340 standard; DNA; 17 BP
             17 TGGCCCGTCATAAGCA 1
                                                                                                                                                                                                                                                      2000US-0234687P
2000US-0236359P
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2001WO-US000666.
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2001WO-US000670.
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                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-533378/51.
                                                                                                                                                                                                                                                                                                                                                                                                                   PENN S G.
HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                      RANK D.
CHEN W.
                                                                                                                                                                                        US2004137589-A1.
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30-JAN-2001;
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05-FEB-2001;
25-MAY-2001;
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σ
                                                                               ACN63340;
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(PENN/)
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(SHAN/)
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                                                   ACN63340
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The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and 65% identity to (S1). A polypeptide of the invention acts as a agonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.

The present sequence represents a 17-mer nucleotide, used in the

This invention relates to a novel method for detecting and distinguishing between colon cell proliferative disorders. Specifically, it comprises contacting genomic DNA isolated from a biological sample with reagents (such as bisulfite) that distinguish between methylated and nonmethylated CpG dinucleotides within at least one target regions of the genomic DNA. The present invention provides genomic regions that include those from ENAJ, COXTB, FTHI, SOXZI, TGFBR2 and H-cadherin genes amongst others, where detection of hypermethylation on these genes indicates the presence of a colon cell proliferative disorder. Furthermore, this method come used to distinguish between one or more of colorectal carcinoma, colon adenoma, inflammatory colon tissue, grade 2 dysplasia colon adenoma, inflammatory colon tissue, grade 2 dysplasia colon adenoma less than 1 cm, grade 3 dysplasia colon adenoma ses than 1 cm, grade 3 dysplasia colon adenoma less than 1 cm, grade 3 dysplasia colon adenoma less than 1 cm, grade 3 dysplasia colon adenoma less than 1 cm, grade 3 dysplasia colon adenoma service of colorectal carcinoma, colon cancer tissue. Accordingly, the methods are also useful for detecting aerodigestive cell proliferative disorders in particular, this method exhibits improved sensitivity, specificity and likely patient compliance. This oligonucleotide is a DNA oligo derived from a gene associated with colon cell proliferative disorders given in an exemplification of the invention. NOTE: There are sequences referred to in this invention that are not provided within the specification and it Detecting and/or detecting and distinguishing between or among colon cell proliferative disorders in a subject by contacting genomic DNA with reagents that distinguishes between methylated and non-methylated CpG DNA oligo of a colon cell proliferative disorder related gene Seg 754. Gaps methylation; cell proliferation; colorectal tumor; inflammation; dysplasia; 88. ; 0 invention for scanning the sequence represented in ACN63102 DB 1; Length 17; Lewin J; Indels Sequence 17 BP; 1 A; 11 C; 1 G; 4 T; 0 U; 0 Other; Sledziewski A, Rujan T, 3, 46.9%; Score 12.2; D 82.4%; Pred. No. 56; iive 0; Mismatches Example 15; SEQ ID NO 754; 399pp; English. 20 BP. 17 23-JUN-2003; 2003US-00602494. 23-JUN-2003; 2003US-00603138. 27-FEB-2004; 2004EP-00090072. 23-JUN-2004; 2004WO-US020336. 06-MAY-2004; 2004EP-00090175 4 CCTCATCGCCCCTTCCT CATCCTCGCCCCCTCCT ADW01436 standard; DNA; 16 (first entry) Conservative Model F, (EPIG-) EPIGENOMICS AG. WPI; 2005-075589/08. Local Similarity nes 14; Conserv colon tumor; DNA gastrointestinal WO2005001141-A2 Lofton-Day C, Distler J; dinucleotides Unidentified. 24-MAR-2005 06-JAN-2005 ADW01436; Query Match ADW01436/c Matches RESULT 9 유 ð

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, G-protein coupled receptor 4; GPR4; haplotyping; polymorphism;
allele-specific oligonucleotide; ASO; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                            Oligonucleotide SEQ ID NO 109216 for detecting SNP TSC0027329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 76; ttive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 109216; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 BP; 2 A; 9 C; 0 G; 2 T; 0 U; 0 Other;
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                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                               07-APR-2000; 2000DE-01019173
                                        ABF09219 standard; DNA; 13
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                                                                                                           (first entry)
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les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation status.
                                                                                                                                                                                                                                                                                       WO200177384-A2.
                                                                                                           21-FEB-2002
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                                                                          ABF09219;
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       RESULT 11
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                         ABF09219
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has not been possible to obtain this sequence data from other sources.
                                                                                                         Gaps
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                                                                       DB 1; Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 109215; 29pp + Sequence Listing; German.
                                                                                                        2; Indels
                                Sequence 16 BP; 4 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
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                                                                   ch
1 Similarity 86.7%; Pred. No. 66;
13; Conservative 0; Mismatches
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ses 12; Conservative
                                                                                                                                       8 ATCGCCCTTCCTAA 22
                                                                                                                                                              15 ATCGCCGCGTCCTAA 1
                                                                                                                                                                                                                                                               ABF09218 standard; DNA; 13
                                                                                                                                                                                                                                                                                                                                   21-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
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                                                                                Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylation status.
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RESULT 14
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                                                                                                                                                                                                                        The invention relates to G-protein coupled receptor 4 (GPR4) gene variants. The data about the GPR4 polynucleotides and polypeptides and the polymorphisms associated with them are useful for haplotyping at the GPR4 locus. Allele-specific oligonucleotide (ASO) is useful as probes and primers for assaying a polymorphism in GPR4 gene. The present sequence is an ASO primer used to detect human GPR4 gene polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoin arthitis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                      Haplotyping, (H1), the G-protein coupled receptor 4 (GPR4) gene of individual, comprising determining which haplotype an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse relA hammerhead ribozyme target sequence (nt. position 1229).
                                                                                                                                                                                                                                                                                                                      42.3%; Score 11; DB 1; Length 15; 84.6%; Pred. No. 91; 1: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 1 Other;
                                                                                                                              Kazemi A, Koshy
                                                                                                                                                                                                     Claim 15; Page 13; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT54899 standard; RNA; 15 BP.
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94US-00218934.
94US-00222795.
                                                                                                        (GENA-) GENAISSANCE PHARM INC
                                                               09-MAY-2001; 2001WO-US015097.
                                                                                    17-MAY-2000; 2000US-0204928P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.0.
                                                                                                                                                                                                                                                                                                                                                                             3 GCCCTTCCTTRG 15
                                                                                                                                                                                                                                                                                                                                                                 11 GCCCCTTCCTAAG 23
                                                                                                                             Duda AE,
                                                                                                                                                  WPI; 2002-097579/13.
                     WO200187904-A2
                                                                                                                             Bentivegna SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-1994;
29-MAR-1994;
04-APR-1994;
  Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9523225-A2
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07-APR-1997
                                          22-NOV-2001
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their cuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well sequences in creasing tolerance to transplanted tissues. The potential immunosuppressive properties of a ribozyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Stinm S, Karpelsky A, Kisich K, Matulic-Adamic J, McGwiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribozymes having modified bases and methods for producing them - for use
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 226; 407pp; English.
94US-00227958
94US-00228041.
94US-00211280.
94US-0029123.
94US-00292620.
94US-00292620.
94US-00392620.
94US-0039363.
94US-00311486.
94US-00311486.
94US-00311486.
94US-0031148711.
94US-003114971.
94US-003114971.
94US-003114971.
94US-003114971.
94US-0031193.
94US-0031193.
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nes 9; Conservative
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                                                                               06-JUL-1994;
15-AUG-1994;
16-AUG-1994;
17-AUG-1994;
19-AUG-1994;
02-SEP-1994;
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03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
04-NOV-1994;
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23-SEP-1994;
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The present sequence represents a preferred target sequence for an enzymatic nuclectic acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences
                                                      Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TWF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karpeisky A, Kisich K, Maulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribozymes having modified bases and methods for producing them - for
                              Mouse relA hammerhead ribozyme target sequence (nt. position 1279).
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                                                                                                                                                                                                                                                                                                                                                   94US-00201109.
94US-00218934.
94US-00224985.
94US-00227958.
94US-00227958.
94US-00211280.
94US-00291433.
94US-00292620.
94US-00291433.
94US-00391439.
94US-00311486.
94US-00311486.
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 (first entry)
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18-MAY-1994;
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16-AUG-1994;
 07-APR-1997
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07-OCT-1994;
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Modak A,
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Tracz D,
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Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; INF-alpha; respiratory syncytial virus; RSv; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosolerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit rell expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential immunosuppressive properties of a ribozyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                       Gaps
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                                                                                                                                                        Score 10.8; DB 1; Length 15;
Pred. No. 99;
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                                                                                                                             Sequence 15 BP; 1 A; 7 C; 2 G; 0 T; 5 U; 0 Other;
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94US-0022795

94US-00227958

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94US-00291932

94US-00291832

94US-00291832

94US-00391839

94US-00311749

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57.1%;
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                                                                                                                                                                      Best Local Similarity 57.1
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
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AAT54889
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10-NOV-1994;

Dudycz LW;

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                                                                                           b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; intercleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; INF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; archerosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                       Ribozymes having modified bases and methods for producing them - for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10.8; DB:
Pred. No. 99;
3; Mismatches
                                                                                                                                                                                                      in inhibiting disease related genes.
                                                                                                                                                                                                                             Claim 2; Page 226; 407pp; English.
94US-00345516.
94US-00357577.
94US-00363233.
95US-00380734.
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                                                                  (RIBO-) RIBOZYME PHARM INC.
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Best Local Similarity 64.3.
Best Joy Similarity 64.3.
Gonservative
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07-APR-1997 (first en
                                                                                                                                                              WPI; 1995-351090/45.
                                                                                              Stinchcomb DT,
            16-DEC-1994;
23-DEC-1994;
30-JAN-1995;
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Modak A,
Tracz D,
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain protential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to leave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential as for increasing tolerance to transplanted tissues. The potential chamited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI filed.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
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                                                                                                                                                                    940S-00224483.
940S-00224483.
940S-00221932.
940S-00291433.
940S-00291433.
940S-00292620.
940S-0039339.
940S-0030339.
940S-00314997.
940S-00314997.
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940S-00314997.
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940S-00314997.
940S-00314997.
                                               95WO-IB000156
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Best Local Similarity 64.3
Matches 9, Conservative
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                                               23-FEB-1995;
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31-AUG-1995
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04-NOV-1994
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Modak A,
Tracz D,
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16-AUG-1
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b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Ravco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                               gene expression; downregulation; interleukin-5; IL-5; ICAN-1; Intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; Philadelphia chromosome; inflammation; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial infarction; stroke; restenosis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                Mouse relA hammerhead ribozyme target sequence (nt. position 326)
                                                                                                                    Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
                                                                                                                                                                                                                                                                                                                                           94US-00201109.
94US-00218934.
94US-00227958.
94US-00227958.
94US-002279611280.
94US-00271280.
94US-00291433.
94US-00292620.
94US-00291433.
94US-00311486.
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94US-00311486.
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                   AAT54850 standard; RNA; 15
                                                             (revised)
(first entry)
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17-AUG-1994;
19-AUG-1994;
02-SEP-1994;
03-SEP-1994;
23-SEP-1994;
                                                                                                                                                                                                                                                       Mus musculus.
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07-APR-1997
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18-MAY-1994;
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11-0CT-1994
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                                          AAT54850;
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Modak A,
Tracz D,
RESULT 17
            AAT54850
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Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.

Claim 2; Page 225; 407pp; English.

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enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NP-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain potential harmerhead and hairph ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their cuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit relA expression, making them potentially useful for treating rheumatorid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential immunosuppressive properties of a ribozyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia; peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor; angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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present sequence represents a preferred target sequence for an
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                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 2 A; 9 C; 2 G; 0 T; 2 U; 0 Other;
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l Similarity 78.6%;
11; Conservative 1
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Best Local Similarity
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to the position of the cleavage site in full length CETP. The ribozyme binds to 5 nucleotides either side of this site, provided the sequence UH is immediately upstream. The ribozymes are able to cleave mRNA from the gene encoding CETP, thereby blocking synthesis and/or expression of the mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway and the inhibited (or eliminated) thereby preventing the reduction in size density of the high density lipoproteins (HDL), prolonging HDL half life, and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP, specifically familial hypercholesterolaemia, atherosclerosis, peripheral vascular disease, hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia, vascular complications of diabetes, transplant, atherectomy and consisty lipoproteins (LDL), and the HDL.LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels.) The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH cribozymes target specific regions of the CETP gene, they have low non-specific activity

41.5%; Score 10.8; DB 1; Length 15; 71.4%; Pred. No. 99; 2; Indels ive 2; Mismatches 2; Indels Sequence 15 BP; 2 A; 9 C; 1 G; 0 T; 3 U; 0 Other; 1 CCACCTCATCGCCC 14 Query Match Best Local Similarity 71.49 warrhes 10; Conservative ઠે

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Gaps

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AAT49762 standard; RNA; 15 BP 1 ccaccuucuceccc 14 (first entry) 02-MAR-1997 AAT49762; AAT49762 셤

Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia; peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor; angloplastic restenosis; low density lipoprotein; diabetes; HDL; human; LDL; ss.

Human CETP HH ribozyme target sequence #930.

Homo

WO9620279-A1

04-JUL-1996

95WO-US016000. 94US-00363240. 11-DEC-1995; 23-DEC-1994;

(RIBO-) RIBOZYME PHARM INC. (WARN) WARNER LAMBERT CO.

Couture L, Stinchcomb

WPI; 1996-321852/32.

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D, Mcswiggen J, Bisgaier C,

New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.

Claim 4; Page 31; 72pp; English

AAT49608-T49863 represent target sequences for the human cholesterol

TS0137). CETP is a 74 kD glycoprotein that facilitates New Figure 150137. CETP is a 74 kD glycoprotein that facilitates New Figure 150137). CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer between plasma lipoproteins. The numbering of the targets refers to the position of the cleavage site in full length CETP. The ribozyme binds to 5 nucleotides either side of this site, provided the sequence UT is immediately upstream. The ribozymes are able to cleave mRNA from the gene encoding CETP, thereby blocking synthesis and/or expression of the mRNA. By inhibiting CETP, thereby blocking synthesis and/or expression of the mRNA. By inhibiting CETP, thereby preventing the reduction in size can be inhibited (or eliminated) thereby preventing the reduction in size and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP, specifically familial hypercholesterolemma, atherocolerosis, peripheral vascular disease, hypercholesterolemma, hyposlphaliopproteinaemia, dyslipidaemia, vascular complications of diabetes, transplant, atherectomy and cangioglastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteins (LDL), and the HDL.LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH HH ribozymes target specific regions of the CETP gene, they have low nonö 13 Death-associated protein 6; DAXX; polymorphism; haplotype pair; human; immune disorder; autoimmune disease; population diversity; ss; paternity testing; anthropological lineage; forensic application; oligonucleotide primer. Sequences AAS04338-AAS04413 represent oligonucleotide primers specific transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-New human death-associated protein 6 (DAXX) gene variants comprising polymorphic sites useful in studying the effect of variation on the biological activity of DAXX and in developing drugs targeting the Gaps ; DB 1; Length 15; Human DAXX DNA allele-specific oligonucleotide primer #10. Stephens JC; 2; Indels Sequence 15 BP; 1 A; 10 C; 1 G; 0 T; 3 U; 0 Other; Choi JY, Denton RR, Nandabalan K, 41.5%; Score 10.8; D 71.4%; Pred. No. 99; tive 2; Mismatches Claim 15; Page 19; 97pp; English. (GENA-) GENAISSANCE PHARM INC. B 05-OCT-2000; 2000WO-US027487. 99US-0157909P. 1 CCACCTCATCGCCC 14 AAS04347 standard; DNA; 15 2 ccaccuucuceccc 15 07-SEP-2001 (first entry) Best Local Similarity 71.4 Matches 10; Conservative WPI; 2001-308220/32. specific activity WO200125245-A2. 06-OCT-1999; 12-APR-2001 AAS04347; Query Match Chew A, protein. RESULT 20 AAS04347/c Homo \$ 셤 8

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comprise one or more most polymorphisms at specific nuclectide positions to form one of nineteen possible polymorphic variants. Associations to a trait and a genotype or a haplotype of the DAXX gene can be identified by comparing the frequency of the genotype or haplotype in a population exhibiting the trait with that of a reference population. A higher frequency in the trait population indicates an association. Methods involving genotyping or haplotyping of the DAXX gene of an individual can lead to prediction of haplotyping of the DAXX gene of an individual can individuals, and may be useful in studying the expression and biological function of DAXX, as well as in developing drugs targeting this protein. Polymorphic variants of DAXX are useful in studying the effect of the affinity of candidate drugs targeting baxX as well as on the binding affinity of candidate drugs targeting DAXX as well as no the binding affinity of candidate drugs targeting and protein. Oblymorphism is also useful for studying population diversity, anthropological lineage, autoimmune diseases and other immune diseases. Polymorphism is also useful for studying population diversity, anthropological lineage, associations between the DAXX genetic variation and a trait such as level of measure binding affinities of one or more candidate drugs targeting the navy variation.
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   a DNA encoding human death-associated protein 6 (DAXX). This DNA may
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99US-016643.
99US-0156236P.
99US-01562467P.
99US-0169100P.
99US-0167100P.
99US-0173612P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 85.7 nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the DAXX protein
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Matches
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2000US-00531025

20-MAR-2000;

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molecules (e.g. ribozymes) to the use of expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding procein-tyrosine-phosphacase-1b, methonine aminopeptidase (MetAP-2), human telomerase (HTER), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor c eceptor-2 (HERZ/C-erbZ/neu), phospholamban (PLN), presentiln-1 (ps-1), presentiln-2 (ps-2), and hepatitis B virus (HBV) proteins The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNazyme motifis. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, clasets, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for an anti-HER2 NCH also are repeated more than once in the specification, but these have
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                      Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 303995 for detecting SNP TSC0020735.
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                                                                                                                                         Chowrira B;
                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the use of enzymatic nucleic acid
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                                                                                                                    Jsman N, Blatt L, Beigelman L, Burgin A,
Aatulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.5%; Score 10.8; D 71.4%; Pred. No. 99; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     different sequences associated with them.
                                                                                                                                                                                                                                                                                                                       Example 7; Page 471; 717pp; English.
                                                                                                                  Blatt L,
                                                                                                                  Usman N, Blatt L
Matulic-Adamic J,
  14-APR-2000; 2000US-0197769P
                                       2000US-00636385
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                                                                            (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                  Mcswiggen J, U
Karpeisky A, M
Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200177384-A2
                                       09-AUG-2000;
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ABI04022/c
ID ABI0403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 308420 for detecting SNP TSC0023007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                      oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 40.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 1.1e+02; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                      Claim 1; SEQ ID NO 303995; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
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                                                                 Berlin K;
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07-APR-2000; 2000DE-01019173.
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                                                                 Piepenbrock C,
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                               (EPIG-) EPIGENOMICS AG
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                                                                                                   WPI; 2001-657177/75
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                                                                 Olek A,
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Claim 1; SEQ ID NO 308420; 29pp + Sequence Listing; German.

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                                   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. AEC00010 -AEC99989, ABH0010-ABH99989 and ABI00010-ABB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequence
                        This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 63253 for detecting SNP TSC0016710.
                                                                                                                                                                                                                                                                                                                                       40.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 1.1e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 91.7
Matches 11; Conservative
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ABC86334 standard; DNA; 13 BP.
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ABC86334/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH99989, ABH00010-ABH99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                             Gaps
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                                                                                                                                                                                                                                                      Oligonucleotide SEQ ID NO 2227 for detecting SNP TSC000901.
                              Query Match 40.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 1.16+02; Matches 11; Conservative 0; Mismatches 1; Indels
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      Sequence 13 BP; 2 A; 0 C; 10 G; 1 T; 0 U; 0 Other;
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ID ABC02236 standard; DNA; 13 BP.
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                                                                                   4 CCTCATCGCCC 15
                                                                                                           CCTCATCCCCCC 1
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic forms part of the printed specification, but
                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                   Oligonucleotide SEQ ID NO 86351 for detecting SNP TSC0021689.
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Pred. No. 1.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                Claim 1; SEQ ID NO 209368; 29pp + Sequence Listing; German.
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                                                               06-APR-2001; 2001WO-IB000713.
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 Homo sapiens.
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useful for diagnosis and cell typing, is
                              designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                               Claim 1; SEQ ID NO 11630; 29pp + Sequence Listing; German.
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Matches 11; Conservative
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABSC99989, ABF00010-ABSP9989 and ABI0010-ABSI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.1e+02;
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Matches 11; Conservative
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Length 13;

Score 10.4; DB 1; Pred. No. 1.1e+02;

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                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Mismatches
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11; Conservative
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                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                    Oligonucleotide SEQ ID NO 2228 for detecting SNP TSC0000901.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a crange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99989, ABF00010-ABE99899, ABF00010-ABE99899, ABF00010-ABE99899, ABF00010-ABE99989, ABF00010-ABE99899 and ABF00010-ABE9989, ABF00010-ABE998999 and ABF00010-ABE9980, ABF00010-ABE998999 and ABF00010-ABE9980, ABF00010-ABE9989999 and ABF00010-ABE9980, ABF00010-ABE9989999 and ABF00010-ABE9980, ABF00010-ABE9980 and ABF00010-ABE9080 and ABF00010-ABE9080 and ABF00010-ABE9980 and ABF00010-ABE9080 and ABF000010-ABE9080 and ABF00010-ABE9080 and ABF000010-ABE9080 and ABF000010-ABE9080 and ABF000010-ABE9080 and AB
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                     Claim 1; SEQ ID NO 171702; 29pp + Sequence Listing; German.
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                                                                                                          Length 13;
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                                                                                                                                        1; Indels
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data for this patent did not form part of the rase obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                   Query Match
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Matches 11; Conservative
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                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
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                                                                                  ABC63237 standard; DNA; 13 BP.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosline methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, oligomers are also used for detecting cell type differentiation. ABC001019989, ABF00010-ABF99899, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF92073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but
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This invention describes novel oligonucleotide primers or peptide nucleic

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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AB157494

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                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                   acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE099999, ABF00010-ABE99999, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 307435 for detecting SNP TSC0022495.
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                                                                                                                                                                                    Claim 1; SEQ ID NO 303994; 29pp + Sequence Listing; German.
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                                                                                                     Berlin K;
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                                        06-APR-2001; 2001WO-IB000713.
                                                             07-APR-2000; 2000DE-01019173
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                     Piepenbrock C,
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                                                                                                   Olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in clearned string but the printed specification, but
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       18
Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                           Claim 1; SEQ ID NO 307435; 29pp + Sequence Listing; German.
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Matches 10; Conservative
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 193907 for detecting SNP TSC0047683.
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ative 0; Mismatches 0;
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ID ABH37230 standard; DNA; 13
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                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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Oligonucleotide SEQ ID NO 237207 for detecting SNP TSC0057853.
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1.3e+02;
thes 0; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 30024; 29pp + Sequence Listing; German.
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                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 133103; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                      38.5%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
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                                                           Sequence 13 BP; 2 A; 7 C; 1 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                           Local Similarity
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                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                         Oligonucleotide SEQ ID NO 51035 for detecting SNP TSC0014276.
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                      ABC51018 standard; DNA; 13
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Best Local Similarity 100.
Matches 10; Conservative
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RESULT 54
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, and ABI00010-ABF99989 and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at
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Best Local Similarity
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Query Match
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                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                Claim 1; SEQ ID NO 133104; 29pp + Sequence Listing; German.
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ö range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers as also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABE9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic oligonucleotides are used for diagnosis and/or prognosis of cancer and a SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps is cytosine .; 0 typing, Oligonucleotide SEQ ID NO 78483 for detecting SNP TSC0019989. Claim 1; SEQ ID NO 78483; 29pp + Sequence Listing; German. Length 13; 38.5%; Score 10; DB 1; Length 13; Indels designed to detect single-nucleotide polymorphisms and methylation status. Sequence 13 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 1 Other; Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other; 38.5%; Score 10; DB 1; Le 100.0%; Pred. No. 1.3e+02; 100.0%; Pred. ... Ä, Berlin BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 ABC78466 standard; DNA; 13 (first entry) Local Similarity 100. Les 10; Conservative Piepenbrock C, 22 1 cccrrccran 10 13 CCCTTCCTAA (EPIG-) EPIGENOMICS WPI; 2001-657177/75. WO200177384-A2. 21-FEB-2002 18-OCT-2001 ABC78466; Query Match Olek A,

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                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.3e+02;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 10; Conservative
             10; Conservative
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                                         1 CCACCTCATC 10
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Oligonucleotide SEQ ID NO 237208 for detecting SNP TSC0057853.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                    Claim 1; SEQ ID NO 80875; 29pp + Sequence Listing; German.
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represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                Oligonucleotide SEQ ID NO 193908 for detecting SNP TSC0047683.
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                                                                                      Query Match 38.5%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 10; Conservative 0; Mismatches 0; Indels
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                                                              Sequence 13 BP; 3 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                          13 CCCTTCCTAA 22
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABP00010-AB199999 and ABI00010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                    Oligonucleotide SEQ ID NO 78484 for detecting SNP TSC0019989.
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ABC78467 standard; DNA; 13
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Best Local Similarity 100. Matches 10; Conservative

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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                                                                   Homo sapiens.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                              Piepenbrock C,
                (EPIG-) EPIGENOMICS AG
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Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer arange of diseases including immune system, gastrointestinal, respiratory, cargiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tapesent the oligomers described in the invention. NOTE: The sequence data for this patent did not form mar of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Score 9.8; DB 1; Length 13;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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RESULT 71 ABF03105

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                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                     Oligonucleotide SEQ ID NO 103102 for detecting SNP TSC0025784.
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Best Local Similarity 84.6
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designed to detect single-nucleotide polymorphisms and cytosine
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84.6%;
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Matches 11; Conservative
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                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastron, respiratory. central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989, ABH0010-ABE99989, ABH0010-ABE99989 and ABI00010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 205672 for detecting SNP TSC0008146.
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Matches 11; Conservative
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                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic
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ID ABF11862 standard; DNA; 13 BP.
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                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 approach the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 111859; 29pp + Sequence Listing; German.
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22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                        Length 13;
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Pred. No. 1.58+02;
2; Indels
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                                                                   Sequence 13 BP; 2 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 84.6%;
Matches 11; Conservative
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ABF42682 standard; DNA; 13
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABI82073 tarpresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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Matches 11; Conservative
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Olek A,
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                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic
  central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated ganomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010 and RE09989, ABF00010-ABF9989, abH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                          onucleotides, useful for diagnosis and cell typing, i detect single-nucleotide polymorphisms and cytosine
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 58775; 29pp + Sequence Listing; German.
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF0010-ABE99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. ö Oligonucleotide SEQ ID NO 142680 for detecting SNP TSC0035782. Claim 1; SEQ ID NO 142680; 29pp + Sequence Listing; German. Length 13; Score 9.8; DB 1; Length 13.
Pred. No. 1.5e+02;
2; Indels Sequence 13 BP; 3 A; 8 C; 0 G; 2 T; 0 U; 0 Other; was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences Berlin BP 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative ABF42683 standard; DNA; 13 (first entry) 10 CGCCCCTTCCTAA 22 1 CCCCCCTACCTAA 13 Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2 Homo sapiens. 21-FEB-2002 18-OCT-2001 ABF42683; olek A, 8888888888888888 ð 셤

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABP9989, ABF00010-ABP9989, ABF00010-ABP9989, ABF00010-ABB9989, ABF00010-ABP9989, ABF00010-ABP9989
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                                          Oligonucleotide SEQ ID NO 160217 for detecting SNP TSC0040348.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fip.wipo.int/pub/published_pct_sequences
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ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancer also used for adiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polyworphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine .; 0 Oligonucleotide SEQ ID NO 160218 for detecting SNP TSC0040348. Claim 1; SEQ ID NO 103101; 29pp + Sequence Listing; German. Claim 1; SEQ ID NO 160218; 29pp + Sequence Listing; German. Length 13; 2; Indels Sequence 13 BP; 2 A; 0 C; 9 G; 2 T; 0 U; 0 Other; Score 9.8; DB 1; Pred. No. 1.5e+02; 0; Mismatches Berlin K; BP. 37.7%; 84.6%; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. ABF60221 standard; DNA; 13 (first entry) 7 CATCGCCCCTTCC 19 Local Similarity 84.6 nes 11; Conservative 13 CATCCCCCATCC 1 Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. methylation status. methylation status. WO200177384-A2 Homo sapiens. 22-FEB-2002 18-OCT-2001. ABF60221; designed Olek A, Best Loca Matches RESULT 91 ઠ 셤

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              represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                      Score 9.8; DB 1; Length 13; Pred. No. 1.5e+02;
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                                                                                                                                                                           2; Indels
                                                                                                       Seguence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
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84.6%;
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                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 109218; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid. (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 targersent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                     Score 9.8; DB 1; Length 13;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                            Sequence 13 BP; 3 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABF46286 standard; DNA; 13 BP.
                                                                                                                                                                                                                                                                                                                                                        37.7%;
84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local S
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ID ABF46
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ngs4.res

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ABH63230;

ABH63230/c RESULT 98

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The present invention relates to expression cassettes comprising a promoter sequence and a promoter polynucleotide with basal promoter activity, where the promoter sequence is operably linked to a activity, where the promoter sequence is operably linked to a heterologous polynucleotide, and when the expression cassette is inserted into a plant, the heterologous polynucleotide is specifically expressed in a suspensor cell and/or basal region of a plant embryo. The invention also provides polynucleotide sequences encoding Scarlet runner bean cassettes of the invention. The expression cassettes of the invention. The expression cassettes comprising promoters and promoter control elements are useful for modulating transcription of genes in a plant suspensor cell and/or basal region of a plant embryo. The present sequence represents a reverse transcriptase (RT)-PCR primer used in the examples of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression cassette comprises promoters with basal promoter activity operably linked to a heterologous polynucleotide, useful for expression genes in suspensor cells in plants and/or basal region of plant embryo.
                                                                                                                                                                                                      Expression cassette; promoter activity; suspensor cell; plant embryo; modulation of gene transcription; Scarlet runner bean; RT-PCR; reverse transcriptase-PCR; primer; transgenic; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEPHA gene transcriptional control region MZF1 binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9.8; DB 1; Length 13;
Pred. No. 1.5e+02;
0; Mismatches 2; Indel8
                                                                                                                                                           Scarlet runner bean forward RT-PCR primer, H-AP56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tatarinova T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 54; 114pp; English.
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ABK87157/c
ID ABK87157 standard; DNA; 13 BP.
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                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA. (CERE-) CERES INC.
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                                                                                                                                                                                                                                                                                                   Phaseolus coccineus
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              WO200244333-A2.
                                                                                                                07-OCT-2002
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                                                                     ABK87157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. X R X B X B X W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                Gaps
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                                                         Query Match 37.7%; Score 9.8; DB 1; Length 13; Best Local Similarity 84.6%; Pred. No. 1.5e+02; Matches 11; Conservative 0; Mismatches 2; Indels
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              Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                               ABH63230 standard; DNA; 13 BP
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                      CCCTTCCTAAGCA 25
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Goldberg RB;

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Gapa

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Human; NEPHA; ephrin receptor; brain; chromosome 1; apoptosis;

RESULT 99

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The invention relates to antisense oligonucleotides (ADM76030 and ADM76031) targeted to the human NEPHA gene (ADM76029), which encodes a novel brain-derived ephrin receptor (ADM76029). The NEPHA protein has 50.7% homology to the human EphA? ephrin receptor and its gene is located on chromosome 1. Ephrin receptors are overexpressed in various cancers and it has been found that inhibition of NEPHA rexpression promotes control (promoter) region (ADM76037); recombinant vectors and host cells control (promoter) region (ADM76037); recombinant vectors and host cells control (promoter) region (ADM76037); recombinant vectors and host cells comprising the NEPHA promoter operably linked to a reporter gene; a method of screening for compounds which inhibit or activate transcription of the NEPHA gene; and pharmaceutical compositions comprising an compression promotes of the natisense oligonucleotides and modulators of NEPHA transcription are cuseful for inducing apoptosis for the treatment and/or prevention of cancers in which NEPHA is overexpressed such as lung cancer, ovarian cancer, breast cancer, breast cancer, breast cancer, bladder cancer, represent transcriptional cancer. Sequences ADM76038-ADM76311
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target, substrate; catalyst, modulation, expression, Raf gene, delivery,
screening; identification; synthesis; deprotection, purification, cancer,
inflammation, psoriasis, non-hepatic ascites; infection, genetic drift;
restenosis, rheumatoid arthritis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                 Novel antisense oligonucleotide useful as anticancer agent for preventing cancer e.g. lung cancer, stomach cancer, breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
drug screening; antisense therapy; gene therapy; cancer; tumour; lung cancer; ovarian cancer; breast cancer; cervical cancer; prostate cancer; bladder cancer; stomach cancer; colorectal cancer; cytostatic; transcriptional control region; promoter; transcription factor binding site; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 1 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 27; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control region of the NEPHA gene.
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                                                                                                                                                                                                                                                                               05-APR-2002; 2002JP-00103497.
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84.6%;
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                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                          JP2003289876-A.
                                                                                                                     Homo sapiens
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A meritor has been developed to the treatment of a mucro capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic comprises: (a) introducing into the system a random library of nucleic caid catalytes (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (D) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endounclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased calls and to determine c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restencesis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and cativity. AAV99922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method has been developed for the identification of a nucleic acid
                                                                                                                                                                                                                                                                                                                                                            Bellon L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                               Burgin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; nicking agent; assay panel; diagnosis; expression pattern;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.7%; Score 9.8; DB 1; Length 14; 84.6%; Pred. No. 1.5e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                        Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Thompson J, Workman CT, Beaudry A, Sweedler D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14 BP; 3 A; 2 C; 6 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                               Mcswiggen JA,
, Beaudry A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used as antiviral agents and synthons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nicking agent target DNA #1026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 179; Page 164; 259pp; English.
                                                                                                                                                                                            97US-0056808P.
97US-0061321P.
97US-0061324P.
97US-0064866P.
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                                                                                                                                    97US-0046059P.
97US-0049002P.
97US-0051718P.
                                                                                                 98WO-US009249
                                                                                                                                                                                                                                                                             97US-0068212P
                                                                                                                                                                                                                                                                                                                     (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                 Beigelman L, Mc
I, Workman CT,
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14 CAACTCATCGGCC
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                  WO9850530-A2
                                                                                               05-MAY-1998;
                                                                                                                                                                                                                                    02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                   Thompson J,
                                                       12-NOV-1998
                                                                                                                                                                                                22-AUG-1997
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                                                                                                                                        09-MAY-1997
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The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a components under nicking agent, and the conditions cause the nicking agent to nick the mucleic acid sample to thus produce a family of initiating of the produce a family of initiating of the conditions cause the nicking agent to nick the coligonucleotide fragments to a characterization process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterizing other DNA molecules e.g., cDNA, and for characterizing other DNA colecules e.g., cDNA, and for characterizing other DNA conformation is useful for identifying the source organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, non-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prockaryotic and eukaryotic species, subspecially useful for identifying prockaryotic and eukaryotic species, subspecies, and especially strains or individuals of the subspecies. It is especially useful for identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for diagnosing bacterial contamination, monitoring quality assurance/quality control of bacterial contamination, monitoring quality assurance/quality control of abboratory tests involving microbiological assays, tracing bacterial contamination and/or outbreaks of bacterial infections, genome mapping, contamination and/or outbreaks of bacterial infections, genome mapping, contamination and/or outbreaks of bacterial infections, genome mapping, corresponds to an example of the recombinant molecules. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying nucleic acid sample source, useful for identifying bacterial strains involved in nosocomial infections, comprises treating the nucleic acid sample with components comprising a nicking agent under nicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
DNA fingerprinting; nosocomial infection; microbiological assay; bacterial contamination; genome mapping; bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresponds to nucleic acid used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          Van Ness LK;
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                                                                                                                                                                                                            29-JAN-2004; 2004WO-US002720.
                                                                                                                                                                                                                                                            29-JAN-2003; 2003US-0443811P
                                                                                                                                                                                                                                                                                                         (KECK-) KECK GRADUATE INST
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                       Galas DJ,
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-581010/56.
                                                                                                                   WO2004067765-A2.
                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     Van Ness J,
                                                                                                                                                                 12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conditions
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The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a nicking agent, and the conditions cause the nicking agent to nick the nucleic acid sample to thus produce a family of initiating only of initiating oligonucleotide fragments to a characterization coligonucleotide fragments. The method is useful for creating an process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterizing other DNA colecules e.g., cDNA, and for characterizing other DNA colecules e.g., cDNA, and for characterizing other DNA colecules e.g., bacterium, fungus, virus, plant, corponism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, conn-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prokaryotic and eukaryotic species, caubspecies, and especially strains or individuals of the subspecies. It is especially useful for identifying different bacterial strains involved in e.g., nosocomial infections. Purthermore, the method is useful for diagnosing bacterial disease in plants and humans, monitoring for bacterial content and/or contamination in the environment, monitoring contamination and plant in the environment, monitoring contamination and plant in the environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying nucleic acid sample source, useful for identifying bacterial strains involved in nosocomial infections, comprises treating the nucleic acid sample with components comprising a nicking agent under nicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial contamination, monitoring quality assurance/quality control of laboratory tests involving microbiological assays, tracing bacterial contamination and/or outbreaks of bacterial infections, genome mapping, monitoring bioremediation sites, and for monitoring agricultural sites for test crops, bacteria and recombinant molecules. This sequence corresponds to nucleic acid used in the method of the invention.
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                     ss; nicking agent; assay panel; diagnosis; expression pattern; DNA fingerprinting; nosocomial infection; microbiological assay; bacterial contamination; genome mapping; bioremediation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.7%; Score 9.8; DB 1; Length 14; 84.6%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                    Van Ness LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 75; 238pp; English.
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                                                                                                                                                                                                                                              29-JAN-2004; 2004WO-US002720.
                                                                                                                                                                                                                                                                                                                                     (KECK-) KECK GRADUATE INST.
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                                                                                                                                                                                                                                                                                                                                                                                 Van Ness J, Galas DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-581010/56.
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                                                                                                                                                        WO2004067765-A2
                                                                                                              Homo sapiens
                                                                                                                                                                                                    12-AUG-2004.
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ABV68451/c
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RESULT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                           Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Hofmann K;
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                                                                                                                                                                                                                                                                                                                                  03-JAN-2001; 2001DE-01000127.
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Local Similarity 90.9%;
les 10; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conradt M,
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                  Human skin EST 6237
                                                                                                                                                                                                                                                                                                                                                                           (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .g. skin cancer.
                                                                                                                                                                                                 WO200253774-A2
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                                                                                                                                                       Homo sapiens.
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disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin
                                                                                                                                                                                                                                                                                                    In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 1.7e+02;
); Mismatches 1; Indels
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90.9%;
20-DEC-2001; 2001WO-EP015179
                                                              03-JAN-2001; 2001DE-01000127
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Best Local Similarity 90.9
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                                                                                                                                                                                                                                                                                                                                                               e.g. skin cancer.
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                                                                                                                                                                                    Petersohn D,
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Disclosure, Page 140, 1345pp, German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of bumans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriais; scleroderma; ichthyosis; atopic dermatitis; acnes; seborncha; lupus erythematosus; rosacca; melanoma; basal call carcinoma; and carcinoma or sarcoma of the sen, can be be used to be seed sequence tag of the invention

Sequence 11 BP; 4 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Gaps ö Length 11; 1; Indels Score 9.4; DB 1; Pred. No. 1.7e+02; 0; Mismatches 1; 36.2%; Local Similarity 90.9 nes 10; Conservative Query Match Best Loca. Matches

8 ATCGCCCCTTC 18 11 ATTGCCCCTTC 1 ઠે 음

AAX77682 standard; DNA; 12 RESULT 107

AAX77682;

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09-AUG-1999 (first entry) N12 active EGS 11.

External guide sequence, EGS; target mRNA; identification; diagnostic; inactivation; essential gene; therapy; ss.

Synthetic.

W09927135-A2

03-JUN-1999

98WO-US024854 97US-00976220 20-NOV-1998; 21-NOV-1997;

98US-0079851P 30-MAR-1998;

(INNO-) INNOVIR LAB INC

Nilsen TW, Robertson HD,

Kindt TJ;

WPI; 1999-357853/30

Identifying and inhibiting functional nucleic acid molecules in cells Example 3; Page 29; 58pp; English. This invention describes a novel method allowing essential or functional genes to be rapidly identified and inactivated. The method is able to firstly identify most of the essential genes in an organism (i.e. a bacteria or a eukaryote) needed for survival, and secondly it provides for reducing or inactivating their expression. The method is able to diagnostic reagents and therapeutics. The method provides a means for identifying essential genes whose sequence is known only as part of a genome with unknown function, as well as a means for identifying functional oligonuclectide molecules. The method involves the use of a nucleic acid molecule comprising (a first reporter gene encoding a fusion protein comprising a protein of interest (itself translated from

an RNA of interest) and a reporter protein, a second reporter gene encoding a second reporter protein, and (c) a targeting gene encoding a functional oligonucleotide molecule such as an external guide sequence (EGS), a ribozyme or an antisense RNA and targeted to the RNA of interest at a site on the first reporter gene able to encode the RNA of interest Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

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Gaps ö Score 9.4; DB 1; Length 12; Pred. No. 1.7e+02; 0; Mismatches 1; Indels 36.2%; 90.9%; 10; Conservative Local Similarity Query Match Matches

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RESULT 108

BP. ABH83039 standard; DNA; 12 ABH83039,

ABH83039;

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(first entry) 22-FEB-2002 Oligonucleotide primer SEQ ID NO 283032 for detecting SNP TSC0011109.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

Claim 1; SEQ ID NO 283032; 29pp + Sequence Listing; German.

methylation status.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

ö Score 9.4; DB 1; Length 12; Pred. No. 1.7e+02; 0; Mismatches 1; Indels 36.2%; Best Local Similarity 90.9 Matches 10; Conservative Query Match

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Gaps

4 CCTCATCGCCC 14

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Wed May 10 10:49:52 2006

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Olek A,
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                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                      central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
                                                                                                                            Oligonucleotide primer SEQ ID NO 276286 for detecting SNP TSC0004140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 307408 for detecting SNP TSC0022484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                              onucleotides, useful for diagnosis and cell typing, detect single-nucleotide polymorphisms and cytosine
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                                                              ABH76293 standard; DNA; 12
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                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                Set of oligonucleotides,
                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
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WPI; 2001-657177/75.
                                                                                                                                                                                                                                                                                                                                                                                     methylation status.
                                                                                                                                                                                                               WO200177384-A2
                                                                                                                                                                                           Homo sapiens.
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Matches 10
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                                                                                   ABH76293;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF0010-ABE99899 and ABI0010-ABE99899. The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                          invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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 07-APR-2000; 2000DE-01019173
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                                                              Piepenbrock C,
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                               (EPIG-) EPIGENOMICS AG.
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                                                                                            WPI; 2001-657177/75.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for diseases in chemically pretreated genomic DNA. The range of diseases including immune system, gastroninestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                          Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
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ABI07294 standard; DNA; 12
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ABI07294
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                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 317750 for detecting SNP TSC0028225.
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     36.2%; Score 9.4; DB 1; Length 12;
al Similarity 90.9%; Pred. No. 1.7e+02;
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            Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
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Best Local Similarity 90.9
Matches 10; Conservative
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RESULT 115

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                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                  Oligonucleotide primer SEQ ID NO 307267 for detecting SNP TSC0022406.
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Matches 10; Conservative
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This invention describes novel oligomuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a crange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABH99989, and ABI0010-ABH32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                       Claim 1; SEQ ID NO 305394; 29pp + Sequence Listing; German.
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Matches 10; Conservative
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                                                                                                                             methylation status.
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ABI13342/c
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Homo sapiens.
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Query Match

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                           36.2%; Score 9.4; DB 1; Length 12; 90.9%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
 Gaps
                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 377399 for detecting SNP TSC0010447.
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                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                         Oligonucleotide primer SEQ ID NO 344659 for detecting SNP TSC0043651.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                      invention describes novel oligonucleotide primers or peptide nucleic
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                           Claim 1; SEQ ID NO 316732; 29pp + Sequence Listing; German.
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90.9%; Pred. No. 1.7e+02;
tive 0; Mismatches 1; Indels
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 1.7e+02;
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                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                         Oligonucleotide primer SEQ ID NO 376045 for detecting SNP TSC0061586.
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                                       ABI76072 standard; DNA; 12 BP.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                  This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 +ABC99989, ABR00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 288035 for detecting SNP TSC0013344.
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                                                                                                                             oligonucleotides, useful for diagnosis and cell typing, ad to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 1.7e+02;
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                                          Berlin K;
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ilarity 90.9%;
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                                          Olek A, Piepenbrock C,
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(EPIG-) EPIGENOMICS AG
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                                                                                                                                                                          methylation status.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequence
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          ABI49799;
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                                                                                                                                                                                                                                                     olek A,
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                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                              Gaps
                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 283033 for detecting SNP TSC0011109.
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         Length 12;
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                            1; Indels
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       Score 9.4; DB 1;
Pred. No. 1.7e+02;
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Beet Local Similarity 90.35,
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                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Hepatotropic; Nephrotropic; Neuroprotective; Vulnerary; Antiinflammatory;
Nephrotropic; Cerebroprotective; ss.
                                                                               Oligonucleotide primer SEQ ID NO 349772 for detecting SNP TSC0046308.
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(first entry)
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ses 10; Conservative
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The present sequence is that of a human connective tissue growth factor (CTGF) cDNA fragment (nucleotides 190-201) that corresponds to a mRNA target of anti-scarring ribozymes of the invention. CTGF is a factor known to be involved in scar formation. The invention relates to ribozymes that specifically target and destroy mRNA sequences encoded by specific CTGF DNA sequences ADU73694-ADU73739 such as the present sequence. The ribozymes can be in hammerhead configuration ADU73740. ADU73741. Methods and compositions for treating scarring conditions associated with increased expression of CTGF are provided, as well as cells containing anti-CTGF ribozymes and vectored anti-CTGF ribozymes suitable for delivery to callular targets capable of CTGF expression. In a claimed method for reducing CTGF mRNA or protein expression in a claimed method for reducing CTGF mRNA or protein expression in a claimed method for reducing CTGF mRNA or protein expression in a claimed method for reducing CTGF mRNA or protein expression in a claim that encodes at least containing an uncleic acid that encodes at least containing an uncleic acid that encodes at least contains and a colling contacted with a vector comprising a nucleic acid that encodes at least contains and acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one ribozyme that specifically cleaves a target RNA sequence encoded by a CTGF gene. The cell may be a fibroblast, and the tissue may be from a subject having, or at risk of developing, a condition causing a scar. The condition is a fibrotic disorder specifically selected from scleroderma, keloids, liver cirrhosis, kidney fibrosis, peritoneal adhesions, tendon adhesions, breast implant capsule adhesions, burn scars, spinal cord injuries, bile duct atresia, subspithelial fibrosis, fibrous dysplasia, and tympanic membrane fibrosis. The condition may also be wound healing following surgery, especially corneal surgery or glaucoma filtering surgery, and the tissue to be treated may be an ocular tissue selected from the cornea, conjunctiva, sclera and trabecular meshwork. Also claimed is a polyzyme that specifically cleaves a target RNA encoded by a CTGF gene and comprises conjoined ribozymes separated by a GCrich stem-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                            New ribozyme specifically cleaving a target RNA sequence encoded by connective tissue growth factor (CTGF) gene, useful for reducing or preventing scarring conditions such as scleroderma and keloids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9.4; DB 1; Length 12;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analyte detection; microarray; probe; ss; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 0 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 18; 58pp; English
                                                                                                                                                                                                                                             Blalock TD;
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                                                                                              30-APR-2004; 2004WO-US013357.
                                                                                                                                            01-MAY-2003; 2003US-0467119P
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Local Similarity 90.9%;
les 10; Conservative
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                                                                                                                                                                                                                                             Lewin AS,
                                                                                                                                                                                             UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                              WPI; 2004-805116/79.
WO2004099372-A2
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                                                                                                                                                                                                                                             Schultz GS,
                                              18-NOV-2004
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The present invention relates to a novel substrate having an oxide layer, which is useful in optically detecting a target material. The thickness of the oxide layer may vary to the wavelength of excitation light used. Also claimed is a method for detecting a target material, comprising immobilizing a probe material on a substrate, reacting the immobilized probe material and the target material, illuminating a reaction product with excitation light, and measuring light emitted from the invention. Comprisited by the excitation light. In an example from the invention, microarrays were fabricated by forming fused silica (SiO2) layers on silicon wafers, followed by linkage with a coupling agent and immobilization of oligonucleotide probes. The microarrays were then incubated with labeled oligonucleotides and exposed to excitation light, and light emitted from the target oligonucleotides with respect to the thickness of the SiO2 layers. ADZ85128-ADZ85203, MODY 3 diabetes-associated probes used with the target sequence of human glyceraldehyde-3-phosphate dehydrogenase (GAPDH), were used to show that when a target coligonucleotide is detected using a microarray including a substrate with an oxide layer a good signal is obtained compared to that with no oxide
                                                                                                                                                                                                                                                               Substrate for use in optically detecting target materials, comprises an oxide layer having thickness that may vary to wavelength of excitation light used.
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 31; 20pp; English.
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                                                                                      22-NOV-2004; 2004US-00994626.
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Atches 10; Conservative
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                    US2005112677-A1.
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                                                   26-MAY-2005
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99JP-00314335.

04-NOV-1999;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                     New inducible eukaryotic promoters containing heavy metal sensitive DNA sequences useful for the production of vectors inducible by gene therapy
                                                                                                                                                                                                                                The present invention provides inducible eukaryotic promoters containir heavy metal sensitive DNA sequences, derived from natural promoters, or of which is shown here. These can be used in the production of vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligonucleotides, useful for diagnosis and cell typing, ied to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide SEQ ID NO 171151 for detecting SNP TSC0009084.
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                                                                                                                                                                                                                                                                                                                                               36.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 1.7e+02; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                   Claim 1; Page 50; 60pp; Japanese.
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                                           (SAKA ) OTSUKA PHARM CO LID.
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                                                                                                      WPI; 2001-308744/32.
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Best Local Similarity
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                                                                            Kataoka K;
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC39989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic
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                                                                                                                Score 9.4; DB 1; Length 13;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 1.7e+02; ative 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 87742; 29pp + Sequence Listing; German.
                                                                                        Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                          ABC87725 standard; DNA; 13
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nes 10; Conservative
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                                                                                                               Query Match
Best Local Similarity
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Oligonucleotide SEQ ID NO 126496 for detecting SNP TSC0031652
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                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 targersent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                             Oligonucleotide SEQ ID NO 126495 for detecting SNP TSC0031652.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 13;
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Pred. No. 1.7e+02;
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90.9%;
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Best Local Similarity 90.9
Then 10; Conservative
                CCACATCGCCC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                   methylation status.
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                                                      RESULT 13
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF9989, ABR00010-ABF9989, ABR00010-ABF9989, ABR00010-ABF9989, ABR00010-ABF9989, ABR00010-ABF9989, and ABIO010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 37116; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                            36.2%; Score 9.4; DB 1; Length 13; larity 90.9%; Pred. No. 1.7e+02; Conservative 0; Mismatches 1; Indels
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                                              Seguence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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Olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABE9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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               range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF9989, ABF00010-ABF99899 and ABI00010-ABF89989 and ABI00010-ABF89989 and ABI00010-ABF89989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
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oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                  Oligonucleotide SEQ ID NO 149605 for detecting SNP TSC0037765.
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                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 149605; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                   Berlin K;
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           21-FEB-2002 (first entry)
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acid (PNA) Oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligometotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABP00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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                                                                                                                                                                                                                                                            Berlin K;
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Matches 10; Conservative
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                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                          Claim 1; SEQ ID NO 205333; 29pp + Sequence Listing; German
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Pred. No. 1.7e+02;
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90.9%;
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Best Local Similarity 90.9
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                   methylation status.
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated ganomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wipo.int/pub/published_pct_sequences
   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABF69493 standard; DNA; 13
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                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 167797 for detecting SNP TSC0010656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 167797; 29pp + Sequence Listing; German.
                        36.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 1.7e+02;
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Sequence 13 BP; 5 A; 1 C; 5 G; 1 T; 0 U; 1 Other;
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                                                                                                                                                              ABF67800 standard; DNA; 13
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                    Query Match
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Matches 10; Conservative
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RESULT 161 ABF69493

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                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                       Oligonucleotide SEQ ID NO 169490 for detecting SNP TSC0042339.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at they printed specification, but fip.wipo.int/pub/published_pct_sequences
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Pred. No. 1.7e+02;
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                                                                                                                                                          Claim 1; SEQ ID NO 5883; 29pp + Sequence Listing; German.
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABR00010-ABE99989, ABR0010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/pub/published_pct_sequences
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                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                    Oligonucleotide SEQ ID NO 97322 for detecting SNP TSC0024141.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleatide nolymershiems (SND)
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                 SEQ ID NO 187480; 29pp + Sequence Listing; German.
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                                                                                                                                                   36.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                    Oligonucleotide SEQ ID NO 74020 for detecting SNP TSC0019042.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                                              uer or origonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                          Claim 1; SEQ ID NO 131881; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.2%; Score 9.4; DB 1; Length 13; Best Local Similarity 76.9%; Pred. No. 1.7e+02; Matches 10; Conservative 1; Mismatches 2; Indels
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                  Piepenbrock C,
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                  Olek A,
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABC0010-ABC9989, ABH0010-ABH99999 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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90.9%;
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Best Local Similarity 90.55,
Conservative
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                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Score 9.4; DB 1; Length 13;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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                          0; Mismatches
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 Query Match 36.2
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10, Conservative
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ABF00945 standard; DNA; 13 BP.

RESULT 178
ABF00945
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                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                          Oligonucleotide SEQ ID NO 100942 for detecting SNP TSC0025123.
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21-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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Matches 10; Conservative
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WPI; 2001-657177/75

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                              Claim 1; SEQ ID NO 112773; 29pp + Sequence Listing; German.
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for diseases including immune system, gastroninestinal, respiratory. central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
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                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                      Oligonucleotide SEQ ID NO 100941 for detecting SNP TSC0025123.
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABP00010-ABH99989 and ABI00010-ABF182073. Tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic
                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                               (EPIG-) EPIGENOMICS AG.
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                                                                                                 WPI; 2001-657177/75
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                                                                 Olek A,
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PMA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from MIPO at the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ngle nucleotide polymorphism, human, diagnosis; PNA; cancer, CNS; nucleic acid; cytosine methylation; cardiovascular; primer; ss;
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                                                                                                                                                                                                                                                                                                                              36.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 1.7e+02;
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Best Local Similarity 90.5-
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                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                              Score 9.4; DB 1; Length 13;
Pred. No. 1.7e+02;
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Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
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This invention describes novel oligomucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                        bet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                   Claim 1; SEQ ID NO 88488; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                Score 9.4; DB 1; Lengtn 15.
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                     Sequence 13 BP; 0 A; 9 C; 0 G; 4 T; 0 U; 0 Other;
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90.9%;
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Best Local Similarity 90.99,
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           WPI; 2001-657177/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at ftp.wipo.int/pub/published_pct_sequences
range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers ea also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence and for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 169489 for detecting SNP TSC0042339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9.4; DB 1; Length 13; Pred. No. 1.7e+02; 1; Mismatches 2; Indels
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1.1 Similarity 76.9%;
10; Conservative 1
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76.9%;
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      21-FEB-2002 (first entry)
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                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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   1; Indels
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Conservative
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Best Local Similarity
Matches 10; Conserv
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Matches
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                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 154545 for detecting SNP TSC0039062.
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                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide SEQ ID NO 47114 for detecting SNP TSC0013556.
                                                                                                                                                                   Claim 1; SEQ ID NO 160495; 29pp + Sequence Listing; German.
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          06-APR-2001; 2001WO-IB000713.
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                                07-APR-2000; 2000DE-01019173
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                                                                             Piepenbrock C,
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                                                                  acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                       Claim 1; SEQ ID NO 47114; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                   36.2%; Score 9.4; DB 1; Length 13; 76.9%; Pred. No. 1.7e+02;
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                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory. central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at five printed specification, but five wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic
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       Berlin K;
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but thouson in electronic format from WIPD at
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36.2%; Scc. 90.9%; Pred. No. ...
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                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                       Oligonucleotide SEQ ID NO 99113 for detecting SNP TSC0024611.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                               Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.2%;
90.9%;
                                                        06-APR-2001; 2001WO-IB000713.
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                                                                                      07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                   (EPIG-) EPIGENOMICS AG
                                                                                                                                                Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-657177/75
                                                                                                                                                                                                                                        methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
 WO200177384-A2.
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   ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine
                                                                                                                                         Claim 1; SEQ ID NO 88487; 29pp + Sequence Listing; German.
Set of oligonucleotides, useful for diagnosis
                                                                      methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences

Sequence 13 BP; 4 A; 0 C; 9 G; 0 T; 0 U; 0 Other;

Gaps ö 36.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 1.7e+02; 1; Indels Mismatches ö Conservative TCCCCCTTCC 19 e 13 rerecerree Query Match Best Local Similarity Matches 10; Conserv ò 셤

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ABF31889 standard; DNA; 13 ABF31889; RESULT 209

BP.

Oligonucleotide SEQ ID NO 131886 for detecting SNP TSC0032929. (first entry) 21-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C, WPI; 2001-657177/75. Claim 1; SEQ ID NO 131886; 29pp + Sequence Listing; German.

bet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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oligomers are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073
-Eppresent the Oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene polymorphism in drug-related genes such as aryl acetylanded deacetylase, arylalkylamine Nacetyl transferase or ATP-binding cassette, sub-family A (ABC1), member 1. The method is useful for analyzing haplotype. The method is useful for estimating the sensitivity or disease of a medicine or a foreign material, for selecting medicine for preventing or treating diseases, for determining appropriate dosage of medicine for preventing or treating disease, for analyzing a drug interaction, and for determining the related polymorphism relative to the sensitivity of the medicine, foreign material or disease. The disease include malignant tumor, immune disorder circulatory disease, metabolic disease, kidney disease, respiratory disease and muscle associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analyzing haplotype, by detecting polymorphism in drug-related genes, electing common polymorphism (CP), building haplotype block using CP, specifying CP within block, specifying tag polymorphism from CP within block.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of analyzing haplotype, by detecting
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm; immune disorder; cardiovascular disease; metabolic disorder; respiratory disease; musculoskeletal disease; renal disease; nephrotropic; endocrine disease; genitourinary disease.
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                                                                                                                                                                  36.2%; Score 9.4; DB 1; Length 13; 76.9%; Pred. No. 1.7e+02; ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human SNP detection related oligonucelotide #470.
                                                                                                                              Sequence 13 BP; 0 A; 6 C; 1 G; 5 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 470; 1290pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito S, Nakamura Y,
                                                                                                                                                                                                                                                                                                                                                                      BP.
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28-MAY-2004; 2004JP-00158717.
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                                                                                                                                                                                                                                                                                                                                                                   ADZ23503 standard; DNA; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                Query Match
Best Local Similarity
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(STAG-) STAGEN CO L
(SEKI/) SEKINE A.
(IIDA/) IIDA A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IIDA/) IIDA A.
(SAIT/) SAITO S.
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Wed May 10 10:49:52 2006

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WO9639195-A2
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                                                                                                                                                                                                                                                                    Glazer PM,
                                                                                                                                       Synthetic.
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                                        AAT70006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ81070 is the supF gene triplex forming mutagenic oligonucleotide pso-AG10. It forms a triplex (a triple stranded nucleic acid) with a specific site on the supF genome, enabling the covalently bound 4'hydroxymethyl-4.5', 8-trimethylpsoralen group to produce a site specific mutation. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mutagenic oligo:nucleotide(s) - having a mutagen incorporated in an oligo:nucleotide which forms a triplex, for site-directed mutagenesis.
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/note= "4'hydroxymethyl-4,5', 8-trimethylpsoralenated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
        related to the sensitivity of a medicine, using a haplotype, without using each single nucleotide polymorphism. The present sequence represents a human SNP detection related oligonucelotide.
                                                                                              Gaps
disease. The method enables analysis of the individual differences
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                                                                                                                                                                                                                                                                                       supF gene; triplex forming mutagenic oligonucleotide; pso-AG10;
4'hydroxymethyl-4,5',8-trimethylpsoralenated; site specific; ss
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                                                                                                                                                                                                                                                                    supf gene triplex forming mutagenic oligonucleotide pso-AG10.
                                                                        36.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 1.7e+02;
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                                                                                             1; Indels
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                                                    Sequence 13 BP; 1 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 5; 72pp; English.
                                                                                                                                                                                          AAQ81070 standard; DNA; 10 BP.
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(first entry)
                                                                      Query Match 36.2
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                2 CCTTCCTAGGC 12
                                                                                                                  14 CCTTCCTAAGC 24
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modified_base
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21-SEP-1995
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                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                               AAQ81070;
                                                                                                                                                                     RESULT 211
                                                                                                                                                                               AAQ81070,
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                                                                                                                                                                                                            Site-directed mutagenesis; triple helix; triplex; psoralen; gene therapy; oncogene inactivation; supF gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homopurine oligonucleotide AG10 (AAT70006) can be linked to psoralen at its 5' end and used to achieve site-specific, targetted mutagenesis of a specific gene. It is based on a homopurine/ homopyrimidine 10-bp motificum at bp 167-176 of the suppr gene. Isea also AAT70005), an E. coliamber suppressor tyrosine tRNA gene. Targetted mutagenesis was achieved by incubating pso-AG10 with supF DNA in vitro to form a triplex at positions 167-176 of the supF gene and bring the tethered psoralen into proximity with the targetted base pair 167 (see also AAT70008). This method of site- directed mutagenesis can be used for gene thereby, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inactivate oncogenes or viral genes, to study DNA repair mechanisms and
to produce transmutated plants and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triple-helix forming oligo:nucleotide linked to a mutagen - useful for site-specific mutagenesis of target gene, e.g. for gene therapy or to inactivate oncogene(s) or viral genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide AG10, which binds triplex target site in supFG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                   Triplex-forming oligonucleotide AG10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 68pp; English.
BP.
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AAT70006 standard; DNA; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                                                                                                                                                      Oligo-nucleotide for targetted mutagenesis of double stranded nucleic acid mol. - by forming triple stranded nucleic acid mol. with target region of double stranded nucleic acid mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss
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                                                                                                                                                                                                                                                                                      Example 1; Fig 1; 29pp; English
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98US-0089844P.
98US-0089853P.
98US-0089878P.
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                                                              03-JUN-1996;
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WO9640898-A1
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19-JUN-1998;
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                               19-DEC-1996
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                                                                                                                                                          Glazer PM;
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Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory coffector proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while cother transcripts correspond to novel genes. Antigen-presenting cell cativation of the cytotoxic immune response, particularly against tumour action of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the WHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory coffectors also being required for the tumour cells, immunostimulatory coffectors also being required for efficient activation of cytotoxic T-lymphocytes (CTMs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in APC; and as hybridisation probes/amplification primers for the capression of these genes betection of the dendritic cell differentially expressed genes in expression of these genes. Cells as belonging to the monocyte lineage. Cells containing these genes cells as belonging to the monocyte lineage. Cells containing these genes cells as belonging to the monocyte lineage. Cells appulation of antigen-specific effector cells) and vectors containing the expression of their encoded proteins, can be used in active immunotherapy. Co-administration of tumour antigens and presentation to endoremous APC and unremense antigen and unremense and unremous antigense 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          presentation to endogenous Apcs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immus effector cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 121; 130pp; English.
                                                     98US - 00899997P
98US - 0089999P
98US - 0090035P
98US - 0090035P
98US - 0090041P
98US - 0090041P
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98US-0089994P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-106077/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROBE/) ROBERTS B L
(SHAN/) SHANKARA S.
                                                                       19-JUN-1998
19-JUN-1998
19-JUN-1998
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Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells. AAZ89342 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). AAZ89342 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and communosasys or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences) particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                         Gaps
                                                                                                                                                                                                                                                                                                                                  Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                         ..
                                                                                                                                                                                                                                                                                                Metastatic breast tumour cell upregulated transcript tag #2259.
   34.6%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                             AAZ83025 standard; DNA; 10 BP.
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98US-0090039P.
98US-0090040P.
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Query Match
Best Local Similarity 100.
Matches 9; Conservative
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(ROBE/)
(SHAN/)
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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA289342 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in metastatic breast tumour cells). AA28677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and creatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences). Particularly an antigen-encoding sequence for use in gene or cell-based vaccines, Polypetides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raishing specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-epecific immune effecter.
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                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Human, metastatic breast tumour tissue; breast cancer, tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                 Metastatic breast tumour cell upregulated transcript tag #431.
                                   34.6%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
Sequence 10 BP; 2 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                  AAZ81197 standard; DNA; 10 BP.
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98US-0089997P.
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                                                                           9; Conservative
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                                     Query Match
Best Local Similarity
Matches 9; Conserv
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(ROBE/) 1
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The invention relates to nucleic acids containing a modified base, especially a substituted vinyl group at the 5-position of a pyrimidine, such that nucleic acids can be reversibly ligated to each other by light-irradiation. The nucleic acids with unique structures can be synthesised for use in gene therapy, DNA computing and immobilisation of nucleic acids. The ligation and immobilisation processes involve the use of light, which is environmentally friendly. The present sequence is that of an oligonucleotide useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                                           Modified base; vinyl group; reversible ligation; irradiation; gene therapy; DNA computing; immobilisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids and methods for reversible ligation using light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S, Yoshino
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100.0%; Pred. No. 2e+
ative 0; Mismatches
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                       AAH79172 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-2000; 2000JP-00067519.
05-JAN-2001; 2001JP-00000750.
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es 9; Conservative
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                                                                                                                                         Oligonucleotide ODN A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito I, Fujimoto K,
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                                                                                                                                                                                                                                       Synthetic.
                                                               AAH79172;
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       AAH79172/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Restriction enzyme; sticky end; nucleic acid fragment; adapator-indexer; nucleic acid characterisation; gene expression pattern analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying nucleic acid fragments in a sample by Fixed Address Analysis of Sequences Tags for cataloging nucleic acids, involves sequence-based capture of indexed fragments on detector array and detecting labels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for identifying nucleic acid fragments in a sample. The method comprises incubating nucleic acid sample with nucleic acid cleaving agents e.g. restriction enzymes that collectively generate sticky ends having different sequences to produce nucleic acid fragments with sticky ends, mixing adapator-indexers with aucleic acid sample and covalently coupling adaptor-indexers to nucleic acid samples. The present sequence is an oligonucleotide used in the method of the present invention. The method may be used for nucleic acid characterisation and analysis, especially for analysis and comparison of
                                                                                                                     Gaps
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                                                                         34.6%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guerra CE, Weber SC,
                                       Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                       AAC80000 standard; DNA; 10 BP.
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                                                       Query Match
Best Local Similarity 100...
Section 9; Conservative
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1es 9; Conservative
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immunotherapy
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Latimer DR;
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0; Indels Length 10;

WO200077214-A2

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RESULT 218

Query Match Best Loca Matches

DB 1; L

99US-00335032

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                               Velculescu V, Vogelstein B, Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 247; 419pp; English.
                                                                                                                                    14-JUN-2000; 2000WO-US016223
                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-061874/07.
                              WO200077214-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cantifungal drugs comprising: (a) contacting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contiguous nucleotides of a NORP gene whose expression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORP gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contiour mucleotides of a NORP gene whose expression is affected by the class of thuse. The drugs whose capression is affected by the class of thuse. The drugs whose capressed genes may be used to identify candidate drugs which affect the cell cycle the cell cycle of a contod comprise of a nord for identify candidate drugs which affect the cell cycle of a cycle and for identification of antifungal drugs, the drugs which affect the cell cycle of a cycle and for identification of antifungal drugs, the drugs which affect the cell cycle of a cycle and for identification of antifungal drugs. The NORP gene is an expressed genes may be used to identify candidate drugs which affect the cell cycle of a cycle and for identification of antifungal drugs.
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                                                                                                                                                                                                                                                                                                                   Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                  Kinzler K;
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                                                                                                                                                                                                               Vogelstein B,
                                                    14-JUN-2000; 2000WO-US016223
                                                                                                      99US-00335032
                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS.
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                                                                                                                                                                                                            Velculescu V,
                                                                                                      16-JUN-1999;
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21-DEC-2000
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log to hase, S phase and G2/M; (2) a method (M2) for screening candidate of cantifungal drugs comprising: (a) contacting a test substance which expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for call; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contioning expression in the yeast cell of at least 1 NORF gene whose contiguous nucleotides of a NORF gene whose contiguous nucleotides of a NORF gene whose contiguous nucleotides of a NORF gene whose contiguous nucleotides as markers of phases of the cell cycle. The expression is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs. Applaysed in the exemplification of the present invention.

AAF31326 to AAF31326 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Matches 9, Conservative
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RESULT 220 AAF40197

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Saccharomyces cerevisiae.

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Cycle and for identification of the present invention cycle in the exemplification of the present invention.
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                                                                                                                                                                                                                               Kinzler K;
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                                                                                                                             14-JUN-2000; 2000WO-US016223.
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                                Saccharomyces cerevisiae.
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linker; PCR primer; ds.
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Best Local Similarity
                                                            WO200077214-A2.
                                                                                                                                                                                                                            Velculescu V,
                                                                                                                                                               16-JUN-1999;
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also cedescribed are: (1) a method (M1) of using NORF genes to affect the cell cycle selected from log thase, 5 phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) munitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell with a candidate drug and contacting expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug contacting a yeast cell with a candidate drug and expression is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which have an event of contiguous may be used to dentify candidate drugs which have a used to setting expressed genes may be used to identify candidate drugs. AAF31268 to AAF44064 crepresent SAGE tags used in the exemplification of the present invention.

Cycle and for identification of antifungal drugs. AAF33268 to AAF44064 crepresent invention. The woramnification of the present invention.
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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
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                                                                                                                                                                                                           Saccharomyces cerevisiae.
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AAD26869
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                            seguence
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                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                           The invention relates to G-protein coupled receptor 4 (GPR4) gene variants. The data about the GPR4 polynucleotides and polypeptides and the polymorphisms associated with them are useful for haplotyping at the GPR4 locus. Allele-specific oligonucleotide (ASO) is useful as probes and primers for assaying a polymorphism in GPR4 gene. The present sequence is a primer used to detect human GPR4 gene polymorphism
                                                                                                                                                                                                Haplotyping, (H1), the G-protein coupled receptor 4 (GPR4) gene of an individual, comprising determining which haplotype an individual.
                         Human; G-protein coupled receptor 4; GPR4; haplotyping; polymorphism;
allele-specific oligonucleotide; ASO; primer; ss.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-canonical zinc finger binding protein; ZFP; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                          34.6%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
        Human GPR4 gene polymorphism detecting primer #10.
                                                                                                                                                                                                                                                                                                          Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc finger protein #5target DNA SEQ ID No 55.
                                                                                                                                                              Koshy B;
                                                                                                                                                              Kazemi A,
                                                                                                                                                                                                                           Claim 17; Page 13; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                            AAL40869 standard; DNA; 10 BP.
                                                                                                                                            (GENA-) GENAISSANCE PHARM INC
                                                                                                        09-MAY-2001; 2001WO-US015097.
                                                                                                                           17-MAY-2000; 2000US-0204928P.
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11-MAY-2001; 2001US-0290716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                              Bentivegna SC, Duda AE,
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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                                                                     WO200187904-A2.
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                                                                                       22-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL40869;
                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 224
                                                     Ношо
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a modified plant zinc finger protein. This zinc finger protein is used to modulated gene expression in a plant cell. Nucleic acid encoding the zinc finger is expressed in plant cells to produce a plant with an altered phenotype relative to the wild-type plant. The altered phenotype is high in nutritional value, yield, stress tolerance, pathogen resistance, resistance to agrochemicals, production of pharmaceutical compounds or production of industrial chemicals. The present sequence is a nucleotide sequence of the gamma tocopherol
Non-canonical zinc finger binding protein for modulating gene expression comprises non-canonical zinc finger components that bind to a target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zinc finger, stress tolerance; pathogen resistance; agrochemical; ds;
gamma tocopherol methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gamma tocopherol methyltransferase target site #5.
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                                                                                                                                                                    Example 7; Page 51; 63pp; English
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11-MAY-2001; 2001US-0290716P.
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Best Local Similarity 100.
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target sequence #4.

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target site in a plant gamma-cocopherol methyl transferase (GMT) gene. The zinc-finger protein of the invention is useful in the production of transgenic plants which have increased vitamin B content and/or altered seed oil content (e.g. increased content of gamma-tocopherol). The present DNA sequence represents a zinc-finger protein target sequence within the Arabidopsis gamma-tocopherol methyl transferase (GMT) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises an engineered zinc-finger protein that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New zinc-finger protein, useful for modulating plant gamma-tocopherol methyltransferase to increase Vitamin E content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triple stranded nucleic acid; triple helix formation; DNA blinding protein; transcription; homologous recombination; DNA triplex; mutagenic repair; repressor gene; proliferation; targeted mutagenesis; DNA repair; Virucide; se.
                                                                                                                                                                                                                                                                   engineered zinc-finger protein; transgenic plant; gamma-tocopherol methyl transferase gene; GMT gene; increased vitamin E content; altered seed oil content; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.6%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                        Arabidopsis gamma-tocopherol methyl transferase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venkatramesh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 37; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jamieson A, Rebar E,
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                                                                                             ADJ78767 standard; DNA; 10 BP.
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04-JUN-2002; 2002US-0385992P.
24-JAN-2003; 2003US-0442470P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     WO2003089452-A2.
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                                                                                                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-2003.
                                                                                                                                      ADJ78767;
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                                                    RESULT 227
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                                                                      ADJ78767,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New gene encoding a protein having ethanolaminephosphate cytidyltransferase activity, useful for treating Zellweger's syndrome, or lipid-related diseases such as cardiovascular diseases and obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a mouse gene encoding a protein having ethanolaminephosphate cytidyltransferase (ET) activity appearing as ADD71226, a degenerate variant of the ET gene, or a sequence that hybridises to the complement of the ET gene under stringent conditions. Also included is a promoter of a human ethanolaminephosphate cytidyltransferase gene appearing as ADD7127. The gene and promoter are useful for producing a transgenic animal, and for identifying, preventing, and treating diseases (by gene therapy) related to inappropriate phosphatidylethanolamine production, e.g. Zellweger's syndrome, or lipid-related diseases such as cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atherosclerosis and obesity. The human ET gene is located on chromosome 17. The present sequence is a human ET gene 5' splice donor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splice donor site; antilipemic; cardiant; anorectic;
phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;
cardiovascular disease; atherosclerosis; obesity; chromosome 17.
                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ethenolaminephosphate cytidilyl transferase; ET; ds;
                                                                                    Query Match 34.6%; Score 9; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2a+02; Matches 9; Conservative 0; Mismatches 0; Indels
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                                         Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ET gene 5' splice donor site from intron 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
methyltransferase gene target site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 6; 22pp; English
                                                                                                                                                                                                                                                                                                                               ADD71287 standard; DNA; 10 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bakovic M, Poloumienko A;
                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-844457/78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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11-AUG-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinagenic composition comprising a single stranded nucleic acid molecule having a sequence that forms a triple caranded nucleic acid molecule with a double stranded target sequence, and a carrier suitable for administration to human or animal cells of an amount of the single stranded oligonuclectide for targeted recombination of a donor nucleic acid into the target sequence, induced by triple helix commation between the single stranded oligonuclectide and the double stranded nucleic acid molecule will activate, inactivate or alter the cortavity or function of the double extranded oligonuclectide and the double stranded nucleic acid molecule will activate, inactivate or alter the activity or function of the double-stranded nucleic acid molecule or the protein it encodes. The triplex forming oligonuclectide and be used to protein it encodes. The triplex forming oligonuclectide can be used to block DNA binding proteins and to block transcription both in vitro and in vitro. It can also be used for promoting and increasing the frequency of recombination resulting in a targeted genetic change in human and calls. The oligonuclectide is useful for mutagenic repair that crancer agent for activating a repressor gene that has lost its ability to captores proliferation. The triplex forming oligonuclectides are also useful as a nesearch tool to cause targeted mutagensis. Targeted mutagenesis is cuseful for targeting a normal gene and for the study of mechanisms such as DNA repair. The triplex forming oligonuclectides can also be used in gene therapy, anti-viral therapeutics, scientific research and genetic cancer argument expairs forming oligonuclectides as a last one set in gene therapy, anti-viral therapeutics, scientific research and genetic centing of cells, animals and plants for research and agriculture. This sequence represents a triplex-forming oligonuclectide on also be used in the forming of the sequence represents a triplex-forming oligonuclectides and agriculture.
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0
                                                                                                                                                                                                                                                           New recombinagenic triple-helix forming oligonucleotide, useful in gene therapy, as anti-viral therapeutics or in genetic engineering of cells, animals and plants for generating of new strains of transmutated animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.6%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 1; 18pp; English.
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                                                                                                                        95US-00476712.
                                                                                          15-OCT-2001; 2001US-00978333
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                                                                                                                                                                    (UYYA ) UNIV YALE
                              US2003232768-A1.
                                                                                                                      07-JUN-1995;
                                                                                                                                       04-OCT-1999;
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                                                            18-DEC-2003
                                                                                                                                                                                                                                                                                                         and plants.
                                                                                                                                                                                                  Glazer PM;
 Synthetic.
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The invention describes an engineered zinc finger protein that binds to a target site in a plant gamma-tocopherol methyl transferase (GMT) gene. Also described are: a fusion polypeptide comprising a zinc finger protein and at least one functional domain, an isolated polymucleotide encoding the zinc finger protein; and an expression vector comprising the isolated polymucleotide. The promoter is tissue specific. The engineered zinc finger proteins are useful for modulating expression in plant cells. This sequence represents an arabidopsis thaliana GMT polymuclootide for which interacting modified plant zinc finger proteins have been designed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New engineered zinc finger protein that binds to a target site in a plant gamma-tocopherol methyl transferase (GMT) gene, useful for modulating expression in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apolipoprotein C-1 (APOC1) primer extension oligonucleotide SEQ ID NO:31.
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engineered zinc finger protein; zinc finger protein; ZFP; gamma-tocopherol methyl transferase; GMT; tissue specific promoter; gene expression modulator; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jamieson A, Rebar E;
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                                                                                                                                         Arabidopsis thaliana
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(JAMI/) JAMIESON A.
(REBA/) REBAR E.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LIGG/) LI G.
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ngs4.res

production inhibiting oligonucleotide SEQ ID NO: 97

(first entry)

AAF16610;

99AU-00000510.

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Cohen N,
                                                 Claim 39; SEQ ID NO 31; 85pp; English.
                   Brain C,
                  Athanasiou M, Bra
            (GENA-) GENAISSANCE PHARM INC
14-JAN-2005; 2005WO-US001307.
      22-JAN-2004; 2004US-0538606P.
                            WPI; 2005-555600/56.
                                           (APOC1) gene.
                   Aerssens J,
                      Judson RS,
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Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Gaps .; 0 34.6%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels 100.0%; Pred. No. Zerrive 0; Mismatches 9; Conservative Best Local Similarity Matches 9; Conserv Query Match

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12 CCCCTTCCT 20 6 CCCCTTCCT

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AAF16610 standard; DNA; 11 BP. RESULT 231 AAF16610/c ID AAF166 XX

20-DEC-2001; 2001WO-EP015178 03-JAN-2001; 2001DE-01000121

11-JUL-2002.

Gastric acid disturbance, gastric reflux, gastritis, dyspepsia, stomach ulcer, duodenal ulcer, Helicobacter pylori, antisense; DNA-RNA hybrid, ss. 24-MAY-2000; 2000WO-AU000498. WPI; 2001-025093/03. WO200071164-A1. (TACH/) TACHAS Homo sapiens. Gastric acid 24-MAY-1999; 13-MAR-2001 30-NOV-2000. Tachas G; ABQ87122; Query Match RESULT 232 ABQ87123 ઠ 셤 The invention relates to a method of determining whether an individual to the invention relates to a marker II comprising determining whether the individual has one or two comples or zero copies of any one of the opportance of the haplotypes in the agone or two copies or zero copies of the determining whether the individual has one or two copies of conset associated with the age of of one or two copies of conset of Albeimer's disease. Also included are: assigning an individual to a first age of onset marker group, comprising determining whether the individual as one copy or two copies of any of the haplotypes; at kit for a serious which individual to the first age of onset marker group if the conset marker II, the kit comprising a set of one or more of conset marker II, the kit comprising a set of one or more of conset marker II, and staesae (AD) in an individual has an age of onset marker I or an age of onset marker II; and choosing a treatment for the individual has conset of Albeimer's disease (AD) in an individual has an age of onset marker I or an age of onset marker II; and choosing a treatment for the individual has an age of onset conset of Albeimer's disease (AD) in an individual has an age of onset conset of Albeimer's disease (AD) in an individual has an age of onset comprising the age of onset of Albeimer's didividual has an age of onset comprising at each or the results of the determining step; an article of manufacture, comprising a population for whom the pharmaceutical formulation is an elective independent, a compound effective in delaying the onset of AD, and where the pharmaceutical formulation is at risk for developing AD and is partially and manufacture, of marker II; an article of manufacture, comprising packaging material and manufacturing drug product comprising comprising one active marker II; an article of manufacture, of marker II; and article of manufacture, of one of onset marker II and manufacturing a drug product comprising compining in a page of onset marker II and manufacturing Determining whether an individual has an age of onset marker I or marker II comprises determining whether the individual has one or two copies or zero copies of any one of the haplotypes in the apolipoprotein C-1 extension oligonucleotide used in haplotype mapping of the APOC1 gene, which maps to chromosome 19q13.2. Denton RR Dain B,

ö The present invention provides oligonucleotides, and methods for their use, which are useful in modulating the action of proteins involved in gastric acid production. The target protein is preferably the histamine H2 receptor or one of the proteins which form part of the gastric proton pump. The sequences and methods of the invention are useful in the treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers, duodenal ulcers and other gastric acid disturbances, most of which are caused by Helicobacter pylori Treating gastric acid disturbance by administering an oligonucleotide which modulates the activity of a polypeptide involved in gastric acid Gaps Human; skin ageing; skin stress; EST; expressed sequence tag; ss. ö 34.6%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels Human skin stress/ageing related EST SEQ ID NO 877. Sequence 11 BP; 4 A; 0 C; 7 G; 0 T; 0 U; 0 Other; Example 3; Page 149; 164pp; English. ABQ87122 standard; cDNA; 11 BP. 10-SEP-2002 (first entry) Best_Local Similarity 100. Matches 9; Conservative production or secretion. 20 10 CCCCTTCCT 2 12 CCCCTTCCT WO200253773-A2 Homo sapiens

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Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                                                                       The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed
                                                                          aging, useful e.g. in based on differential gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to in vitro identification (M1) of genes expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                                                                                                                                                                                         2e+02;
                                                                         Identifying genes involved in skin stress and screening for cosmetic or therapeutic agents,
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llarity 100.0%; Pred. No. 2e+
Conservative 0; Mismatches
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                                Hofmann
                                                                                                                     Claim 8; Page 73; 325pp; German.
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                                Petersohn D, Conradt
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           (HENK ) HENKEL KGAA
                                                     WPI; 2002-528865/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human skin EST 9394
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                                                                                                  expression.
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Matches
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ö The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriamis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; cosceas, melanoms; basal cell carcinoma, and carcinoma or sarcoma of the in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin promotes skin homeostasis or that can be used for treating skin ichthyosis; atopic dermatitis; annohum, psoriasis; scleroderma; ichthyosis; atopic dermatitis; annohum; basin stythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss. In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Gaps The present sequence is that of a human expressed sequence tag ö 34.6%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 2e+02; cive 0; Mismatches 0; Indels Seguence 11 BP; 2 A; 0 C; 6 G; 3 T; 0 U; 0 Other; Hofmann K; Disclosure; Page 48; 1345pp; German. ABV63036 standard; cDNA; 11 BP. 20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127 (first entry) Σ 9; Conservative of the invention σ ო WPI; 2002-590638/63. (HENK) HENKEL KGAA. CCACCTCAT Query Match Best Local Similarity CCACCTCAT Human skin EST 822 e.g. skin cancer. WO200253774-A2. Homo sapiens. 21-OCT-2002 Petersohn D, 11-JUL-2002. ABV63036; ч 11

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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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                                                              Human skin EST 5495
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                                                                                                                                  Homo sapiens.
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                  ABV67709;
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                  Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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            34.6%; Score 9; DB 1
100.0%; Pred. No. 2e+
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Hofmann K;
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                                                                                                                                        ABV64187 standard; cDNA; 11 BP.
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Best Local Similarity 100.v.
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9; Conservative
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                                                         12 CCCCTTCCT 20
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                                                                                                                                                                                                            Human skin EST 1973
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Hofmann K;

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(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psorlaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                         Disclosure; Page 176; 1345pp; German.
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Matches 9; Conservative
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ABV67709 standard; cDNA; 11 BP.

RESULT 236 ABV67709 ID ABV6770

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                               e.g. skin cancer.
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                  Hofmann K;
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                                                                                                                                                                                  Claim 24; Page 250; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV62656 standard; cDNA; 11 BP
                                       20-DEC-2001; 2001WO-EP015179.
                                                          03-JAN-2001; 2001DE-01000127
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                                                                                                  Petersohn D, Conradt
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Best Local Similarity
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                                                                                                                                                             .g. skin cancer.
WO200253774-A2
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                    11-JUL-2002
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Matches
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ö The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriacis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss. Gaps ; 34.6%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 2e+02; Live 0; Mismatches 0; Indels Sequence 11 BP; 0 A; 7 C; 1 G; 3 T; 0 U; 0 Other; Hofmann K; Disclosure; Page 37; 1345pp; German. Claim 24; Page 264; 1345pp; German. ABV70457 standard; cDNA; 11 BP. 20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127 21-OCT-2002 (first entry) Conradt M, 9; Conservative

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This invention describes a novel in vitro method for identifying genes
that are significant for facial skin in humans. The method comprises
recovering, from facial skin, a first mixture of genetically expressed
(transcribed and optionally translated) factors (i.e. proteins, mRNA or
their fragments), recovering a second, similar mixture from some other
thuman tissue, preferably skin from a protected area, especially from the
breast and subjecting the mixtures to serial analysis of gene expression
tromedial skin and the other tissue. The invention also describes an
in vitro method for determining homeostasis of human facial skin; a test
kit which comprises a soild support (flexible or rigid) on which are
immobilised probes that bind specifically to the factors of interest and
a bisochip for determining homeostasis of human facial skin; a test
kit which comprises a soild support (flexible or rigid) on which are
immobilised probes that bind specifically to the factors of interest and
a bisochip for determining homeostasis of human facial skin; a test
cosmetic and pharmaceutical agents for use against disorders or
disturbances of the homeostasis of human skin and a screening method for
identifying cosmetic and pharmaceutical agents. The method allows
condition of as many as possible of the genes important for facial
skin and thus of a very wide range of potential therapeutic and cosmetic
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promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                  Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                           Local Similarity 100.
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This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises crecovering, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other thuman tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different converted skin and the other tissue. The invention also describes and in vitro method for determining homeostasis of human facial skin; a test kit which comprises a solid support (flexible or rigid) on which are invention are also used in a method which determines activity of the invention are also used in a method which determines activity of the invention are also used in a method which determines activity of disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows cometic agents capture and commetic agents in and thus of a very wide range of potential therapeutic and cosmetic agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention.
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agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention
                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; serial analysis of gene expression; SAGE; biochip; cosmetic; pharmaceutical; ds.
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                                                                                               Length 11;
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agents, based on differential expression analysis.
                                                       Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                         34.6%; Score 9; DB 1
100.0%; Pred. No. 2e+
tive 0; Mismatches
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Best Local Similarity
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homeostasis;
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                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 318871 for detecting SNP TSC0028928.
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     DB 1; Le.._
No. 2e+02;
0; Indels
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                 34.6%; Score 9; DB 1
100.0%; Pred. No. 2e+
ive 0; Mismatches
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                                                                                                                                                                                                  ABI18898 standard; DNA; 12
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Query Match
Best Local Similarity 100.
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Matches 9; Conservative
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                                                                                  12 CCCCTTCCT
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                                                                                                                                                                   RESULT 242
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 295660 for detecting SNP TSC0016678.
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This invention describes novel oligonucleotide primers or peptide nucleic
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            Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 100.0%; Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designed to detect methylation status.
                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                 SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 302250 for detecting SNP TSC0019887.
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                                                                                                           ABI02277 standard; DNA; 12
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                  11 CCACCTCAT
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ABI31343
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acid (BNA) oligomers for detecting single nucleotide polymorphisms and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF0010-ABF99989, ABF0010-ABF999899, ABF0010-ABF99989, ABF0010-ABF99999, ABF0010-ABF99999, ABF0010-ABF99999, ABF0010-ABF99999, ABF0010-ABF9999, ABF0010-ABF99999, ABF0010-ABF9999, ABF0010-ABF9999, ABF0010-ABF9999, ABF0010-ABF9999, ABF0010-ABF9999, ABF0010-ABF9999, ABF0010-ABF9999, ABF0010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphysms (SNP)
                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 331316 for detecting SNP TSC0036120.
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Best Local Similarity 100.0%; Pred. No. 2e-
Matches 9; Conservative 0; Mismatches
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cyclosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABH00010-ABH99999 and ABH00010-ABH32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                Berlin K;
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                 07-APR-2000; 2000DE-01019173
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                                                                              Piepenbrock C,
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                                              (EPIG-) EPIGENOMICS AG
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                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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     Claim 1; SEQ ID NO 292092; 29pp + Sequence Listing; German.
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Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 362364 for detecting SNP TSC0053186.
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                                                       34.6%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 34.6%; Score 9; DB 1; Length 12; Local Similarity 100.0%; Pred. No. 2e+02; nes 9; Conservative 0; Mismatches 0; Indels
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Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
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                                                                                                                         9; Conservative
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                                                                                        Local Similarity
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                                                              Query Match
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                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                   Oligonucleotide primer SEQ ID NO 296570 for detecting SNP TSC0017152.
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Pred. No. 2e+02;
0; Mismatches 0; Indels
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                 ABH96577 standard; DNA; 12 BP
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Best Local Similarity
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    ABH96577,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms are from WIPPO at
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ative 0; Mismatches
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Best Local Similarity
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Homo sapiens.
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oligonucleotides are used for diagnosis and/or prognosis of cancer and
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                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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Berlin K;
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Piepenbrock C,
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                                            WPI; 2001-657177/75
                                                                                                                     designed to detect methylation status.
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Matches 9; Conserv
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                          Oligonucleotide primer SEQ ID NO 379937 for detecting SNP TSC0063546.
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                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 368994 for detecting SNP TSC0057391.
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    Pred. No. 2e+02;
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                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                             ligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
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                                          07-APR-2000; 2000DE-01019173
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                                                                                                                             of oligonucleotides,
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hes 9; Conservative
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                                                                                  Olek A, Piepenbrock C,
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                                                                                                                                                   methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073
                                                                                                                                                                                                                                   acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABR99989, ABR0010-ABR99899, ABR0010-ABR99899 and ABI0010-ABR3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                       Claim 1; SEQ ID NO 324895; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0
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                                                 methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 319500 for detecting SNP TSC0029262.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                34.6%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 2e+02; vative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2e+02;
Live 0; Mismatches 0; Indels
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                               34.6%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 2e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 351281 for detecting SNP TSC0047204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 339949; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                        Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
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                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
(EPIG-) EPIGENOMICS AG.
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                                                                                        Olek A,
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15-OCT-1992;
07-DEC-1992;
07-DEC-1992;
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Matches
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                THE LEAN TO SERVE TO 
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 +ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                    34.6%; Score 9; DB 1; Length 12; 100.0%; Pred. No. 2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                               Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
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9205-00882714
9205-00882823
9205-00882886
9205-00882888
9205-00882881
9205-00882921
9205-00883923
9205-00883923
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92US-00884436.
92US-00884521.
92US-00923738.
92US-00935854.
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92US-00884333.
92US-00884422.
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26-AUG-1992;
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14-MAY-1992
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Triplex formation; DNA detection; triple helix; identification; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences for enzymatic RNA molecules. The RNA molecules are complementary to a substrate binding region in the specified gene target. They also have enzymatic activity, in that they specifically cleave RNA in the target. The ERNA interfere with viral replication and therefore have anti-viral properties. They can be used to attenuate viruses to be used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                               Enzymatic RNA molecules - used to inhibit viral replication, infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences (AAQ52923-Q53037) are pref. herpes simplex virus target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triple helix third strand of 23S rRNA gene nucleotides 5444-5455.
                                                                                                                                                                                                                                   Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecek JJ;
Mamone JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%; Score 8.8; DB 1; Length 12; 75.0%; Pred. No. 2.2e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 1 A; 9 C; 1 G; 0 T; 1 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 15; 287pp; English.
92US-00948359.
92US-00963322.
92US-00987129.
92US-00987130.
92US-00987133.
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                                                                                                                                                                          (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                             and gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-130384/11.
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                                                                                                                       07-DEC-1992;
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triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex etability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test of sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand etructure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting cenes for ribosomal RNA) in clinical samples, but also detection of concogenes and Hepatitis B virus
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                                              The present sequence represents a polynucleotide that is able to form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          system used for the selection of polypeptides displayed in a
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer used to bind the Stoffel fragment of DNA polymerase I.
                                                                                                                                                                                                                                                                                                                                                 Score 8.8; DB 1; Length 12; Pred. No. 2.2e+02;
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             Disclosure; Col 23-24; 168pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 38; 64pp; English.
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98GB-00010228.
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Matches 10; Conservative
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modified_base
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13-MAY-1998;
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               The method is used to select for viruses displaying desired polypeptides. The methods may also be used for the identification of interacting protein elements, and for the selection of a repertoire of polypeptides which interact with a selected polypeptide and/or repertoire. Primers AAZ45532-34 were used to select DNA polymerases for catalytic activity, using protease-cleavable helper phage of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
proteolysis. The method reduces background in phage display techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 300302 for detecting SNP TSC0018963.
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Pred. No. 2.2e+02;
                                                                                                                                                                                 Score 8.8; DB 1; Length 12;
Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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                                                                                                                                                Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
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83.3%;
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Best Local Similarity 83.3%;
Matches 10; Conservative C
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                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                            Oligonucleotide primer SEQ ID NO 287738 for detecting SNP TSC0013227.
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                                                                                       ABH87745 standard; DNA; 12 BP.
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                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 313798 for detecting SNP TSC0025975.
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                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 344922 for detecting SNP TSC0043771.
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                                                                                                  designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                  Claim 1; SEQ ID NO 344435; 29pp + Sequence Listing; German.
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Pred. No. 2.2e+02;
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83.3%;
06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 83.3
Matches 10, Conservative
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                                                                Piepenbrock C,
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                                           (EPIG-) EPIGENOMICS AG
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                                                                Olek A,
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                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABF82073 the preparent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 344922; 29pp + Sequence Listing; German.
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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83.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 320903 for detecting SNP TSC0029956.
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                                                              33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; ive 0; Mismatches 2; Indels
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33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                           Local Similarity 83.3
10; Conservative
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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010 appresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 302104 for detecting SNP TSC0019796.
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ABI02131 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
 central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                          WO200177384-A2
                       Homo sapiens.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 327842; 29pp + Sequence Listing; German.
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Berlin K;
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Piepenbrock C,
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Olek A,
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ABH78360/c
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                   Gaps
                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 314759 for detecting SNP TSC0026548.
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
 Score 8.8; DB 1; Length 12;
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83.3%;
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                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                             Oligonucleotide primer SEQ ID NO 315967 for detecting SNP TSC0027203.
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABR0010-ABR99999 ABN0010-ABR99999 ABN0010-ABR99999 ABN0010-ABR99999 and ABN0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par to f the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                             invention describes novel oligonucleotide primers or peptide nucleic
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
                                                                               Claim 1; SEQ ID NO 323187; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                   represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 350201 for detecting SNP TSC0046561.
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Best Local Similarity 83.3%;
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ID AB17;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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cytosine
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22-FEB-2002
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                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastroninestinal, respiratory, caltomers are also used for detecting cell type differentiation. ABC00010 oligomers are also used for detecting cell type differentiation. ABC0001 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                    Claim 1; SEQ ID NO 362746; 29pp + Sequence Listing; German.
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07-APR-2000; 2000DE-01019173
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                                            Piepenbrock C,
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                      (EPIG-) EPIGENOMICS AG
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                                            Olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ABH99872 standard; DNA; 12
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ABI57677 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 349377 for detecting SNP TSC0046101.
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                                                               Query Match 33.8%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 2.2e+02; Matches 10; Conservative 0; Mismatches 2; Indels
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                     Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                         Oligonucleotide primer SEQ ID NO 357650 for detecting SNP TSC0007066.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomecleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABR00010-ABH99989 and ABI00010-ABR182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                  Sequence 12 BP; 1 A; 10 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                           SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 328615 for detecting SNP TSC0034416.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 280327; 29pp + Sequence Listing; German.
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                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                               Oligonucleotide primer SEQ ID NO 329701 for detecting SNP TSC0035095.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 278152 for detecting SNP TSC0005715. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

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                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                            Claim 1; SEQ ID NO 278152; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                   33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                        Sequence 12 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
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methylation status.
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ABI03578/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 306913 for detecting SNP TSC0022244.
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                                                                                                                                                                   Score 8.8; DB 1; Length 12;
Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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                                                                                                                     Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
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83.3%;
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Best Local Similarity 83.3°
Matches 10, Conservative
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Best Local Similarity 83.5.
Local 10; Conservative
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WO200177384-A2
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                                Homo sapiens.
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ABIS9490/
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                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                      Oligonucleotide primer SEQ ID NO 334701 for detecting SNP TSC0038351.
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 334701; 29pp + Sequence Listing; German.
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                                     ABI34728 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                                                            ABI34728;
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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es 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                       Claim 1; SEQ ID NO 359463; 29pp + Sequence Listing; German.
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                             Olek A, Piepenbrock C,
(EPIG-) EPIGENOMICS AG.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR0010-ABP3989 and ABI0010-ABR3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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83.3%;
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Best Local Similarity 83.3
Matches 10, Conservative
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ABH66893/
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Homo sapiens.
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                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                  Gaps
                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 319294 for detecting SNP TSC0029155.
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          Length 12;
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       Score 8.8; DB 1;
Pred. No. 2.2e+02;
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ftp.wipo.int/pub/published_pct_sequences
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1 Similarity 83.3%;
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      Query Match
Best Local
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ABH98731 standard; DNA; 12

RESULT 313

ABH98731

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                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 298724 for detecting SNP TSC0018250.
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83.3%;
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Matches 10; Conservative
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 2.2e+02;
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WO200177384-A2
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ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The SNP, single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Oligonucleotide primer SEQ ID NO 370744 for detecting SNP TSC0058361. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine . 0 Claim 1; SEQ ID NO 370744; 29pp + Sequence Listing; German. German 33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; Ative 0; Mismatches 2; Indels Claim 1; SEQ ID NO 314756; 29pp + Sequence Listing; Sequence 12 BP; 3 A; 5 C; 2 G; 2 T; 0 U; 0 Other; Berlin K; ABI70771 standard; DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 22-FEB-2002 (first entry) 10; Conservative 3 ACCTCATCGCCC 14 1 ACATCATCGCGC 12 ΰ (EPIG-) EPIGENOMICS AG Piepenbrock methylation status. WPI; 2001-657177/75 methylation status. Local Similarity

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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABC99899, ABF0010-ABC99899, ABF0010-ABC99899, ABF0010-ABC99899, ABF0010-ABC99899, ABF00010-ABC99899, ABF00010-ABC99899, ABF00010-ABC99899, ABF00010-ABC99899, ABF00010-ABC99899, ABF00010-ABC99999, ABF00010-ABC99999, ABF00010-ABC99999, ABF00010-ABC99999, ABF00010-ABC99999, ABF00010-ABC99999, ABF00010-ABC99999, ABF00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC999999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC999999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC9999999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC99999, ABC00010-ABC999999, ABC000010-ABC999999, ABC000010-ABC999999, ABC000010-ABC999999, ABC000010-ABC9999999, ABC0000000000-
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 295712 for detecting SNP TSC0016696.
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                                                                                                                                                                                                                                                                                                           33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                            Sequence 12 BP; 0 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 abS09989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formal from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 314753 for detecting SNP TSC0026548.
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                                                                                                           BP.
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                                                                                                         ABI14780 standard; DNA; 12
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                CCCCTCCTAAAC 12
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
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Query Match 33.8%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 2.2e+02; Matches 10; Conservative 0; Mismatches 2; Indels

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ABI50312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; se; central nervous system; gastrointestinal; respiratory; immune; metabolic
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Oligonucleotide primer SEQ ID NO 286583 for detecting SNP TSC0012738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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Matches 10; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotide are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 349107; 29pp + Sequence Listing;
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                                                                                                                                     Berlin K;
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                               This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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Claim 1; SEQ ID NO 350285; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                   Score 8.8; DB 1; Length 12;
Pred. No. 2.2e+02;
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Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
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                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                               Oligonucleotide primer SEQ ID NO 356323 for detecting SNP TSC0050058.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cortral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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83.3%; Pred. No. 2.2e+02;
tive 0; Mismatches 2; Indels
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Homo sapiens.
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oligonucleotides are used for diagnosis and/or prognosis of cancer and
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                                                                                                                                                                                                                                                                                                                                                                            acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomerlectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                     invention describes novel oligonucleotide primers or peptide nucleic
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
                                                            of oligonucleotides, useful for diagnosis and cell typing, is igned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                     Claim 1; SEQ ID NO 281811; 29pp + Sequence Listing; German.
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33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
   Berlin K;
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Piepenbrock C,
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                              WPI; 2001-657177/75
                                                                            designed to detect amethylation status.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invantion. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fip.wipo.int/pub/published_pct_sequences
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Best Local Similarity 83.33
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33.8%; Score 8.8; DB 1; Length 12;

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                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 368210 for detecting SNP TSC0056866.
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33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                     Indels
Pred. No. 2.2e+02;
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          83.3%;
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                                         13 CCCTTCCTAAGC 24
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          Best Local Similarity
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                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
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                                                                                 Oligonucleotide primer SEQ ID NO 270998 for detecting SNP TSC0002355.
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                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 333
                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99999, ABE00010-ABE99999, ABH00010-ABE99999, and ABI00010-ABI99999 and ABI00010-ABI99999. represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                             to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing,
                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 335615; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 1 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                            Berlin K;
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                           06-APR-2001; 2001WO-IB000713
                                                          07-APR-2000; 2000DE-01019173
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                            Piepenbrock C,
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                                                                                         (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                             methylation status.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                     Claim 1; SEQ ID NO 371049; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.8; DB 1; Length 12; Pred. No. 2.2e+02; 0; Mismatches 2; Indels
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 304348 for detecting SNP TSC0020881.
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33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                            33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02;
                                                                                                                      2; Indels
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                                                                   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                                                       10; Conservative
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1 CCATCCTAATCA 12
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                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 337282 for detecting SNP TSC0039782.
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designed to detect single-nucleotide polymorphisms and cytosine
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BP.
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ABI37309 standard; DNA; 12
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovaerular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC001016-ABC9989, ABR00010-ABH99989 and ABI00010-ABH92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                            Berlin K;
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                                                                      Homo sapiens
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Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation, ABC0010-ABC9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 348072 for detecting SNP TSC0010192.
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                                                                                                               ligonuclectides, useful for diagnosis and cell typing, i
to detect single-nuclectide polymorphisms and cytosine
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                                                                                                                                                                             Claim 1; SEQ ID NO 292113; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                               Set of oligonucleotides, useful for
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                                               Piepenbrock C,
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               (EPIG-) EPIGENOMICS AG.
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                                                                                WPI; 2001-657177/75
                                                                                                                                               methylation status.
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                                               olek A,
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ABI48099/c
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ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989, and ABI00010-ABE9989 and ABI00010-ABE90010 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 354578 for detecting SNP TSC0049156. Gaps oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. .; 0 Claim 1; SEQ ID NO 354578; 29pp + Sequence Listing; German. 33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; 2; Indels Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other; 0; Mismatches Berlin K; ABIS4605 standard; DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 (first entry) Best Local Similarity 83.3 Matches 10, Conservative 10 CGCCCCTTCCTA 21 Olek A, Piepenbrock C, 12 CTCCTCTTCCTA 1 (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. WO200177384-A2. Homo sapiens, 22-FEB-2002 18-OCT-2001 Query Match RESULT 339 ABIS4605

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                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 322792 for detecting SNP TSC0031068.
                                                                   Gaps
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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                             Score 8.8; DB 1; Length 12;
Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
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83.3%;
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                               Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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es 10; Conservative
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methylation status.
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RESULT 341

ABI58281

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The invention relates to novel species-specific identification of orthopoxviruses by preparing a biochip with immobilized oligonucleotides on a gel micromatrix on a glass support, amplifying a crmB gene fragment by two-stage asymmetric PCR using a fluorescence-labelled primer, hybridizing the resulting single-stranded DNA on the biochip by incubation in a sealed chamber, and detecting fluorescence and comparing the hybridization pattern with standards. The method is used for species-specific identification of orthopoxviruses, including variola, monkeypox, compox, vaccinia and rabbitpox viruses. This primer is general for
                                                                                                                                                                                                                                                                                                                                                                          Species-specific identification of orthopoxviruses comprises hybridizing crmB gene fragments on a biochip bearing typing oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosomal abnormality, maternal locus; genetic disorder; foetus; mutation; translocation; transversion; monosomy; trisomy 21; chromosome 21; Down's Syndrome; anueoplodies; chromosome addition; chromosome addition; chromosome amplification; chromosome translocation; chromosome rearrangement; single nucleotide polymorphism detection; SNP detection; pregnant female; PCR; primer; so.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; tive 0; Mismatches 2; Indels
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(VEKT=) VEKTOR VIROLOGY & BIOTECH RES CENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 9; 18pp; Russian.
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                                                                                                  26-NOV-2001; 2001WO-RU000507
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11-MAR-2002; 2002US-00093618.
08-MAY-2002; 2002US-0378354P.
                                                                                                                                                                                                                                                                                   Schelkunov SN;
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         WO2003046221-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP)
                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                   Oligonucleotide primer SEQ ID NO 358254 for detecting SNP TSC0007531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD53808 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-2000; 2000DE-01019173.
ABI58281 standard; DNA; 12
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 CCTTCCTAAGCA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                     WO200177384-A2.
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                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                      22-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004
                                           ABI58281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Best Loca Matches

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RESULT 342

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Gaps

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ADR98329,
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                                                                                                                                                                                                                                                                                            It can be used to detect any alterations in a gene sequence, especially single nucleotide polymorphisms (SNPs), and may be used to detect numerous abnormalities simultaneously, for example if several SNPs are associated with a particular disease. The method provides a rapid, noninvasive method for determining the sequence of DNA from a foetus using sample from a pregnant female, for example to detect genetic disorders as above or to determine if a foetus is a carrier of a disease or
                                                             Detection of chromosomal abnormalities e.g. Down's Syndrome, non-
invasively in a fetus, comprises forming a ratio of amounts of alleles at
a locus of interest and a different heterozygous locus.
                                                                                                                                                                                                                    disorders,
                                                                                                                                                  abnormalities by determining the sequence of alleles of a locus of interest from template DNA, determining which alleles are present and comparing to amounts of alleles at a different, selected heterozygous locus (for example on another chromosome or a maternal locus); relative amounts are expressed as a ratio indicating presence or absence of the abnormality. The method is useful for the detection of genetic disorders especially in a foetus, including chromosomal abnormalities and mutations, for example translocations, transversions, monosomies, trisomies (for example trisomy 21 in which an additional copy of chromosome 21 results in Down's Syndrome) and other anueoplodies, deletions, amplifications, translocations and rearrangements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                          This invention relates to a novel method of detecting chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; nicking agent; assay panel; diagnosis; expression pattern; DNA fingerprinting; nosocomial infection; microbiological assay; bacterial contamination; genome mapping; bioremediation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 33.8%; Score 8.8; DB 1; Length 12; Local Similarity 83.3%; Pred. No. 2.2e+02; tes 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 12 BP; 6 A; 1 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                Example 13; Page 266; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nicking agent target DNA #245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galas DJ, Van Ness LK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2004; 2004WO-US002720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR32704 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KECK-) KECK GRADUATE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        predisposed to a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TCGCCCCTTCCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 TTGCCCCTTTCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-581010/56.
                                   WPI; 2003-845073/78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Ness J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-2004
              Dhallan R;
                                                              Detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR32704;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 344
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The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a components under nicking conditions cause the nicking agent to nick the nucleic acid sample to thus produce a family of initiating considered in a subjecting one or more members of the family of initiating oligonucleotide fragments to a characterization process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterizing other DNA conformation and section of a useful for identifying the source organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, con-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prokaryotic and eukaryotic species. Chingerprinting DNA to identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for diagnosing bacterial disease in plants and humans, monitoring for diagnosing bacterial disease in plants and humans, monitoring for contamination, monitoring quality assurance/quality control of bacterial contamination, monitoring quality assurance/quality control of contamination and/or outbreaks of bacterial infections, genome mapping, monitoring bioremediation sites, and for monitoring agricultural sites for test crops, bacteria and recombinant molecules. This sequence corresponds to nucleic acid used in the method of the invention.
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Identifying nucleic acid sample source, useful for identifying bacterial strains involved in nosocomial infections, comprises treating the nucleic acid sample with components comprising a nicking agent under nicking conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SNP TSC08701940 multiplex PCR primer #1.
                                                                                                                                                                                                                          Example 1; Page 75; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2004 (first entry)
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nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCACCTCATCGC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004079011-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-2004.
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WPI; 2004-677127/66.

Ouery Match
Best Local Similarity 83.3. 8

9 TCGCCCCTTCCT 20

ADS09006; RESULT 346 ADS09006/

This invention describes a novel method for detecting a chromosomal choromality in a sample which comprises determining the sequence of alleles of a locus of interest in a sample from template DNA where alleles of a locus of interest in a sample from the plant of the locus of determining the sequence of the alleles comprises amplifying the locus of contracts in a sample from the determining the sequence of the alleles comprises amplifying the locus of contracts of the sequence of the alleles comprises amplification, ligase chain reaction, rapid amplification strand displacement amplification or splice overlap extension Exp. preferably contracts and ligase chain reaction, rapid amplification, strand displacement amplification or splice overlap extension contracts. Fragmented amplification for the sequence of the sequenc Detecting a chromosomal abnormality, e.g. translocations, transversions, monosomies, trisomies, aneuplodies, deletions, or arrangements, comprises determining the sequence of alleles of a locus of interest in the sample primer used to amplify the human SNP TSC08701940 Example 13; Page 249; 429pp; English. from template DNA.

Gaps ; 0 33.8%; Score 8.8; DB 1; Length 12; 83.3%; Pred. No. 2.2e+02; ive 0; Mismatches 2; Indels Sequence 12 BP; 6 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

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12 TIGCCCTTICE 1

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ADS09006 standard; DNA; 12 BP. 02-DEC-2004 (first entry) Human DNA PCR primer #353. X8X4X8X

Human; PCR; primer; 88; nucleic acid detection; cell lysis; bronchus; blackens, bladder; breast; bronchus; colon; kidney; liver; lung; oesophagus; gall bladder; ovary; pancreas; stomach; cervix; thyroid; prostate; skin; small cell lung cancer; squamous cell carcinoma; leukaemis; lymphoma; myelodysplastic syndrome; fibrosarcoma; rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma; schwannoma; melanoma; seminoma; teratocarcinoma; osteosarcoma.

Homo sapiens.

WO2004078994-A2.

16-SEP-2004.

01-MAR-2004; 2004WO-US006337.

28-FEB-2003; 2003WO-US006198.

(RAVG-) RAVGEN INC.

Dhallan R;

WPI; 2004-662434/64.

Detecting presence or absence of nucleic acid, containing mutation, involves isolating nucleic acid from sample containing cell lysis inhibitor, and detecting presence or absence of nucleic acid.

Example 13; Page 258; 440pp; English.

The invention relates to a method for detecting a nucleic acid, involving isolating a nucleic acid from a sample, where an agent that impedes cell isolating a nucleic acid from a sample, where an agent that impedes cell that was added to the sample, and detecting the presence or absence of the nucleic acid. The invention also relates to a method for detecting the nucleic acid. The invention a sample of a pregnant female. The nucleic acid contains at least one mutation chosen from a single point mutation, adeletion, a family at frameshift, a truncation, adeletion, an insertion, arransversion. The method is useful for detecting cutations, and a transversion. The method is useful for detecting cutations, and a transversion. The method is useful for detecting cutations, and a source chosen from bacteria, protozoa, molds, yeasts, plants, humans, conn. humans, multi-cellular parasites, animals and archaebacteria. The method is useful for detecting, diagnosing or monitoring a disease such as cancer chosen from carcinoma of the bladder, breast, bronchus, colon, kidney, liver, lung, oesophagus, gall bladder, ovary, pancreas, stomach, cervix, thyroid, prostate and skin, small cell lung cancer, aguamous cell carcinoma, haematopoietic tumours of lymphona, haematopoietic tumours of lymphona, haematopoietic tumours of lymphona, haematopoietic tumours of myeloid lineage, acute and chronic myelogenous leukaemias, myelodysplastic syndrome and promplemed correct betakenia, tumours of the central and peripheral nervous system, chabitomyosarcoma, tumours of the central and peripheral nervous system, chaptering reservance to the entral and schwannoma, mellod, maniform, myelod, myelod, myelod, mye monitoring response to treatment chosen from surgery, radiation, lifestyle change, dietary protocol and supplementation and administration of a drug is chosen from chemotherapeutic agents, antibacterial agents, anti-lifungal agents, targeted-cancer drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents. This sequence represents a PCR primer used in the scope of the invention.

Sequence 12 BP; 6 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

ö Score 8.8; DB 1; Length 12; Pred. No. 2.2e+02; 0; Mismatches 2; Indels 33.8%; 83.3%; Query Match 33.8 Best Local Similarity 83.3 Matches 10, Conservative

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12 rrgccccrrrcr 1 9 TCGCCCCTTCCT

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Gaps

ADU73727;

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RESULT 347

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CCCCTTCCCGAG 12
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Best Local Similarity
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                                                                                                                                                                                                                              25-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09515177-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1995.
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20-MAR-1996
                                                                                                                                                                               AAQ95491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a human connective tissue growth factor (CTGF) cDNA fragment (nucleotides 589-600) that corresponds to a mRNA target of anti-searring ribozymes of the invention. CTGF is a factor known to be involved in scar formation. The invention relates to ribozymes that specifically target and destroy mRNA sequences encoded by specific CTGF DNA sequences ADU73094-ADU73799 such as the present sequence. The ribozymes can be in hammerhead configuration ADU73740-CC ADU73741. Methods and compositions for treating scarring conditions associated with increased expression of CTGF are provided, as well as cells containing anti-CTGF ribozymes and vectored anti-CTGF ribozymes contistable for delivery to cellular targets capable of CTGF expression. In a cell, a claimed method for reducing CTGF mRNA or protein expression in a cell, a claimed method for reducing CTGF mRNA or protein expression in a cell, a contacted with a vector comprising a nucleic acid that encodes at least cone ribozyme that specifically cleaves a target RNA sequence encoded by a CTGF gene. The cell may be a fibroblast, and the tissue may be from a cubic thaving, or at risk of developing, a condition causing a scar. The condition is a fibrotic disorder selected from scleroderma, keloids, condition is a fibrotic disorder selected from scleroderma, teloids, claver capaule adhesions, burn scars, spinal cord injuries, bile contained in the condition may all subcome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                             Connective tissue growth factor; CTGF; scarring; Dermatological; Hepatotropic; Nephrotropic; Neuroprotective; Vulnerary; Antiinflammatory; Nephrotropic; Cerebroprotective; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surgery, especially corneal surgery or glaucoma filtering surgery, and the tissue to be treated may be an ocular tissue selected from the cornea, conjunctiva, sclera and trabecular meshwork. Also claimed is a polyzyme that specifically cleaves a target RNA encoded by a CTGF gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New ribozyme specifically cleaving a target RNA sequence encoded by a connective tissue growth factor (CTGF) gene, useful for reducing or preventing scarring conditions such as scleroderma and keloids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                   Connective tissue growth factor target for anti-scarring ribozyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 34; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blalock TD;
                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2004; 2004WO-US013357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2003; 2003US-0467119P.
                                            ADU73727 standard; cDNA; 12
                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UYFL ) UNIV FLORIDA
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                                                                                                                                               10-FEB-2005
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Improving efficacy of alpha-helical cytokine(s) - esp. useful for prevention and/or reduction of the severity of neurological conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ95491 is a murine tis11 sequence which resembles the ciliary neur trophic factor response element (CNTF-RE) core (tis11 is a promoter CNTF responsive genes). AAQ95491 is used in a claimed compsn. for improving the efficacy of alpha-helical cytokines, useful for the treatment of neurodegenerative disorders, e.g. Alzheimer's disease
                                                                                                                                                                                       Murine tis11; CNTF responsive genes; alpha-helical cytokines; ciliary neurotrophic factor; response element; CNTF-RE; neurodegenerative disorders; promoter; Alzheimer's disease; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                             Murine tisll sequence resembling the CNTF-RE core.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frank DA;
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AAQ95491 standard; cDNA; 10 BP.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                              New non-pathogenic HIV-1 strain carrying a deletion in its nef gene LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
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Pred. No. 2.5e+02;
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AUSTRALIAN RED CROSS SOC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 190; 301pp; English.
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                              95WO-AU000063
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90.0%;
                                                                                    94AU-00003864
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94AU-00000284
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                                                                                                           21-FEB-1994;
23-DEC-1994;
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23-DEC-1994;
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more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ991019-Q97106) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The responds to nucleotides 1-10 of the nef gene (AAQ96141). The response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel method for the detection of plant pathogenic strains of fungine 5. Septoria nodorum, S.tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijiensis, M.musicola or Fusarium app, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 185, 5.88 and 288 ribosomal RNA genes by the primers AAQ94359-93 and AAT05357-72. These primers are derived from the ITS sequences of these fungi (AAT05394-TD5404 and AAQ94398) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAT05399-93 in colourimetric assays. The primers and ITS DNAs can be used for the detection of specific fungal pathogen isolates and in monitoring disease development in plant populations. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant pathogen; fungue; Septoria nodorum; Septoria tritici; Fusarium; Pseudocercosporella herpotrichoides; Mycosphaerella fijiensis; PCR; Mycosphaerella musicola; amplification; primer; ribosomal RNA gene; internal transcribed region; strain; capture; colourimetric assay; isolate; development; population; random amplified polymorphic DNA; ss.
                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1
LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
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                                                                                                                                                                                                                                                                                                        32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                        Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
                                                          Page 189; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Setoria nodorum RAPD primer OPE-12.
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                                                        Claim 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT35710-T35738 represent amplification primers used in a random amplified polymorphic DNA (RAPD) reaction on V.dahiae DNA. These sequences were used to isolate the sequence represented by AAT35706 for use in the diagnostic assays of the invention. The qualitative assays of the invention. The qualitative assays of the invention comprise analysing a sample for the presence of the sample to the infected by V.dahilae. A quantitative assay of the invention, comprises taking a sample and isolating nucleic acids from it. A sequence that acts as an internal standard (see AAT3570*) is added to the isolated nucleic acids. The internal standard competes with the V.dahilae sequence for the PCR primers used in the reaction (such as the sequence for the PCR primers used in the reaction of the internal standard is a different size to the amplified portion of the internal standard is a different size to the amplified portion of the internal standard is a different size to the amplified portion of the internal field that is going to be used for growing potatoes. These assays are faster and more accurate than methods based on culturing soil samples in selective media. The assays can also distinguish between V.dahilae and V.albo-atrum. By using these assays, unnecessary soil
                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                              RAPD; random amplified polymorphic DNA; diagnostic assay; quantitative; PCR; primer; qualitative; soil sample; agricultural field; potatoe; V.albo-atrum; soil fumigation; amplify; polymerase chain reaction; ss.
                                                                                                                     Gaps
primers AAT05373-7 were obained from purchased random amplified polymorphic DNA (RAPD) primer libraries and used to PCR amplify ITS sequences in conjunction with the primers AAQ94390-3. This primer amplified a 2.2 kb region from S.nodorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assay for Verticillium dahliae - by amplification of specific DNA
                                                                                                                      .
0
                                                                                           32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02;
                                                                                                                     1; Indels
                                                                  Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                     Primer E12 for V.dahliae RAPD reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                         AAT35730 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Col 9; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00335565
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                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                     9; Conservative
                                                                                                                                                                       10
                                                                                                                                              6 TCATCGCCCC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-299849/30.
                                                                                                                                                                       1 TTATCGCCCC
                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1994;
                                                                                                                                                                                                                                                                                              08-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                             US5527671-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German TL,
                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                               RESULT 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAV62567 to AAV62571 represent random amplified polymorphic DNA (RAPD) primers used in the course of the invention for detection of Septoria species. The invention provides a DNA molecule isolated from the ribosomal RNA gene region of a fungal pathogen, where the DNA molecule consists of an internal transcribed spacer (ITS) sequence selected from ITS2 and ITS2 of Fusarium quaminearum, Pusarium moniliforme, Septoria avenae or Microdochicum nivale. A method for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F. svenaceum and M. nivale isolates is also provided which comprises isolating DNA from a plant leaf infected with at least one of the above pathogens and amplifying parts of the ITS sequence of the pathogen (s) by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The pathogen(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusarium culmorum, Fusarium graminearum, Fusarium moniliforme, plant, Septoria avenae, Microdochicum nivale, Fusarium poae, fungal pathogen, random amplified polymorphic DNA, PCR, nucleic acid detection, RAPD,
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosomal RNA; Fusarium avenaceum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR using specific primers from within these sequences. The pathogs are detected by visualising the amplified part of the ITS sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA isolated from fungal RNA, and its internal transcribed spac
sequence - used for detecting fungal pathogens in plant tissue.
                                                  Score 8.4; DB 1; Length 10;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8.4; DB 1; Length 10;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Septoria nodorum species specific RAPD primer OPE-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcribed spacer; ITS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Col 19; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-00722187.
                                                  32.3%;
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                        Query Match
Best Local Similarity 90.v.,
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  AAV62569 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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                                                                                                                                                                                     TTATCGCCCC
                                                                                                                                                        6 TCATCGCCCC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5814453-A.
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                                                                                                                                                                                                                                                                                                                                                                                     AAV62569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beck JJ;
                                                                                                                                                                                                                                                                                     RESULT 353
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identification; bacteria; oncogene; virus; ds.
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                                                                                                                                                                                                                                                                                                                                                                                              Nilaparvata lugens Stall rice. The method comprises: (1) amplification of a DNA fragment by PCR using a PCR marker and detection of the resistance, in which a DNA fragment being specifically amplified in a species having a gene (bph-2) resistant to Nilaparvata lugens Stal. using a genome DNA of rice as a template and 1.3 KDp in total with a base sequence shown by sequence 1 (AAZOB315). comprising 300 bases at 3'-terminal, respectively; and (2) a PCR marker comprising 290 bases at 3'-terminal, respectively; and (2) a PCR marker comprising a sense primer of base numbers shown in sequence 3 (AAZOB314) and antisense primer of base numbers shown in sequence 5 (AAZOB314). The present invention also describes a primer for PCR using rice genome of sequences 9, 10 or 11 (AAZOB314), respectively, for detection of the resistance. The method is used for the simple detection of resistance to Nilaparvata lugens Stal
                                                                                                                           Nilaparvata lugens Stal; rice; detection; resistance; PCR marker; bph-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                             Detection of resistance to Nilaparvata lugens Stal. rice - using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                    A method has been developed for the detection of resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triple-helix forming region; Triplex formation; DNA detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triple helix forming nucleotides 1410-1419 of 23S rRNA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                                                                       Nilaparvata lugens Stal. rice PCR primer sequence #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                  Example; Page 11; 15pp; Japanese.
                                       AAZ08344 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX14836 standard; DNA; 10 BP.
                                                                                                                                                                                                                                          98JP-00010845.
                                                                                                                                                                                                                                                                98JP-00010845,
                                                                                                                                                                                                                                                                                     (AICH-) AICHI KEN PREFECTURE
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                           amplification techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 TCATCGCCCC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTATCGCCC 10
                                                                                                                                                                                                                                                                                                           WPI; 1999-486354/41.
                                                                                                                                                                         Nilaparvata lugens.
                                                                                                                                        PCR primer; ss
                                                                                                                                                                                                                                         22-JAN-1998;
                                                                                                                                                                                                                                                               22-JAN-1998;
                                                                                                                                                                                             JP11206376-A
                                                                                  13-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1999
                                                                                                                                                                                                                   03-AUG-1999
                                                                                                                                                             Synthetic
                                                            AAZ08344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX14836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                   RESULT 354
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AAX14836/c
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Matches
                             AAZ0834
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The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human dendritic cell SAGE tag, SEQ ID NO:1798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Col 21-22; 168pp; English.
                                                                                                                                                                                                                                                                                                                            (PROF-) PROFILE DIAGNOSTIC SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ79370 standard; DNA; 10 BP.
                                                                                                                                                                                              93US-00173489.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             Hepburn AG, Wang C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-130384/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 TCCCCCTTC
Escherichia coli.
                                                                                                                                                                                              22-DEC-1993;
                                                                                                                                                                                                                                                               29-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9965924-A2
                                                                JS5861244-A
                                                                                                                              19-JAN-1999
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AAZ79370
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Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proceins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while correspond to novel genes. Antigen-presenting cell cher transcripts correspond to novel genes. Antigen-presenting cell cher transcripts correspond to novel genes. Antigen-presenting cell cher transcripts correspond to novel genes. Antigen-presenting cell cativation of the cytotoxic immune response, particularly against tumour cells, immunostimulatory cofactors also being required for activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for sefficient activation of cytotoxic 7-lymphocytes (CTLs). Nucleic cild sefficient activation of cytotoxic 7-lymphocytes (CTLs). Nucleic cild sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; no screen for an APC; and as hybridisation probes/amplification primers for the dagnosis, prognosis and monitoring of differentially expressed genes in complex. Complex of the dendritic cell differentially capteres and monitoring of diseases related to abnormal expressed of antigen specific effector cells) and vectors containing them are used in active immunotherapy (or to stimulate production of a prognesus and monitoring of diseases. Cells as belonging to the monocyte lineage. Cells containing these genes copially of antigen specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and presentation of co-stimulatory signals, migration of chemoty secretio
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98US-0089844P.
98US-0089873P.
98US-0089921P.
98US-0089932P.
98US-0089937P.
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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                                                                                          32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                               Sequence 10 BP; 0 A; 8 C; 0 G; 2 T; 0 U; 0 Other;
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recruitment of immune effector cells
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                                                                                                                      Local Similarity
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Sequences AAZ7573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding compared timenosticulatory cofactor protains which are preferentially or differentially expressed in monocyte-derived dendritic cells compared differentially expressed in monocyte-derived dendritic cells compared (expressed sequence tags) which were previoually unknown to be correspond to novel genes. Antigen-presenting cells (APC)-associated costimulatory factors play an important role in the correspond to novel genes. Antigen-presenting cells (APC)-associated costimulatory factors play an important role in the corpus of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MEC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone complex) and subsequent recognition by T-cell receptors is alone complex) and subsequent recognition by T-cell receptors is alone complex, and subsequent recognition by T-cell receptors is alone complex, and subsequent recognition by T-cell receptors is alone complex, and subsequent recognition by T-cell receptors is alone complex, and subsequent recognition by T-cell receptors is alone complex, and subsequent recognition by T-cell receptors is alone complex, and subsequent recognition of differential uses. They may be used in vaccines to induce an immune response, particularly cagainst tumour antigen, to modulate expression of differentially expressed genes for against that modulate expression of differentially expressed genes. Cc against that modulate expression of diseases related to abnormal expression of these genes. Detection of diseases related to abnormal expression of these genes. Detection of diseases related to abnormal expression of these genes. Detection of the dendritic cells of the mare used in active immunotherapy. Call of the compleximation of antigen-specific effector cells of the production of conformous APCs and upregulates the APCs for the presentation of c
                           Isolated polynucleotides differentially expressed in antigen-presenting
                                                                  cells, useful in gene vaccines against cancer.
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32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
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Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L.

08-DEC-1998

(SHAN/) SHANKARA S.

Claim 1; Page 99; 130pp; English.

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Human dendritic cell SAGE tag, SEQ ID NO:1195.
AAZ78767 standard; DNA; 10 BP.
                  10-APR-2000 (first entry)
         AAZ78767;
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WO9965924-A2.

23-DEC-1999

Homo sapiens

18-JUN-1999;

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Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proceins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previoually unknown to be cother transcripts correspond to novel genes. Antigen-presenting cell cother transcripts correspond to novel genes. Antigen-presenting cell cother transcripts correspond to novel genes. Antigen-presenting cell activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone activated a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient to activate a robust cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of diseases related to abnormal expression of these genes, or of their encoded proteins, call differentially expressed genes, or of their encoded proteins, call so the dending to the dending coll and vectors containing these can be used in gene therapy. Co-administration of tumour antigens and continue therapy. Co-administration of tumour antigens and presentation to endogenous APC ensemble or the procession of the dending presentation to costimulatory signals, migration to T cell-rich sites, presentation to creaminatory signals, migration to T cell-rich sites.
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secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells
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                                 Length 10;
                               Query Match 32.3%; Score 8.4; DB 1; Length 10 Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                    Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
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activation of the cytoxic immune response, particularly against tumour activation of the cytoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for against a tumour antigen; to modulate the genotype of an APC; to screen for against a tumour antigen; to modulate in modulate expression of differentially expressed genes in APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing the associated characterismination general energy of the manner administration of tumour antigens and antigen and active farmines admines antigen antigen antigen and antigen antigen and antigen antigen and antigen and antigen antigen and antigen antigen and antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression) tags used to identify mana transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the
Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells). AAZ8942 that are preferentially transcribed in metastatic breast tumour cells). AAZ8942 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, monitoring and creatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcribts are used to direct expression, in selected cell types, of c.g. therapeutic genes (also ribozymes or antisense sequences).

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                                                  98US-0089853P.
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non-metastatic breast tumour tissue; gene therapy; anticancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 61; 219pp; English.
             98US-0089997P.
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                                                                                                                                                                                                                                                                                                 AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.
                                                                                                                                                                                                                         Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            Claim 1; Page 70; 219pp; English.
                                            98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
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                       99WO-US013647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                           Shankara S;
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                                                                                                                        (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                                                                                                                     treatment of cancer.
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                                                                                                                                                 SHAN/) SHANKARA S.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotherapy
                                                          19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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                       18-JUN-1999;
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                                                19-JUN-1998
23-DEC-1999
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that are preferentially transcribed in the metastatic breast tumour cells). AAZ80767 to AAZ80341 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). AAZ80342 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downrequlated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic and isolate populations of educated, antispense sed for adoptive cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 180; 219pp; English.
                                                                                                                                                                                                                                                            98US-0089997P.
98US-0090039P.
98US-0090040P.
98US-0090041P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SHAN/) SHANKARA S.
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WO9965928-A2
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antimetastatic; vaccine; diagnosis; ss.
                                    Homo sapiens
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19-JUN-1998;
19-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotides differentially expressed between metastic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                         98US-0089853P.
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                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer.
                                                                                                                                                                                                                                                        SHANKARA S.
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19-JUN-1998;
19-JUN-1998;
Ното варіепв
                            WO9965928-A2
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                                                                                                                                                                                                                                      (ROBE/)
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AAZ85435/c
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells). AAZ83942 corresponding to distinct transcripts that are preferentially transcribed in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These crissue (i.e. are downrequiated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and creatment of breast cancer, particularly where metastatic. Diagnosis is compounds that modulate expression of the transcripts are potentially cuseful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter
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                                                                                                               98US-0089997P.
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99WO-US013647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of cancer.
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thas are preferentially transcribed in the metastatic breast tumour thas are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ8342 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially useful for transment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).

CC oparticularly an antisen-encoding sequence for use in gene or cell-based corrines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter and isolate populations of educated, antigen-specific immune effecter cells, and these used for adoptive
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Human; metastatic breast tumour tissue; breast cancer; tag; primer;
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                non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 74; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ84149 standard; DNA; 10 BP.
                                                                                                                                                                                                        98US-0089853P.
98US-0089997P.
98US-0090039P.
98US-0090040P.
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90.0%;
                                                                                                                                                                         99WO-US013647
                                                                                                                                                                                                                                                                               98US-0090041P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Roberts BL, Shankara S;
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                                                                                                                                                                                                                                                                                                                (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-106079/09.
                                                                                                                                                                                                                                                                                                                                                   SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mmunotherapy
                                                                                                      WO9965928-A2.
                                                                     Homo sapiens
                                                                                                                                                                         18-JUN-1999;
                                                                                                                                                                                                                                             19-7UN-1998;
                                                                                                                                                                                                                              9-JUN-1998
                                                                                                                                                                                                                                                                               19-JUN-1998
                                                                                                                                       23-DEC-1999
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                                                                                                                                                                                                                                                                                                                                    ROBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 367
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that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells. AAZ86071 represent tags corresponding to distinct transcribes that are to AAZ86677 represent tags corresponding to distinct transcribes that are to AAZ86677 represent tags corresponding to distinct transcribes that are corresponding to distinct transcribes that are corresponding to non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and corresponding to breast cancer, particularly where metastatic Diagnosis is compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic agenes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                               Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
Metastatic breast tumour cell downregulated transcript tag #3383
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98US-0090039P.
98US-0090040P.
98US-0090041P.
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                                                                                                                                                                                                                                                                                                                                                         GENZYME CORP. ROBERTS B L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer.
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CTCCCCTTCC
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                                                                                                                                            WO9965928-A2
                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                         (GENZ )
(ROBE/)
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Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag; granulocyte-macrophage colony-stimulating factor; characterisation; GM-CSF; identification; diagnosis; gene specificity; oncogenesis; disease onset mechanism; genetic disease; drug development; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes 100 human genes, which are expressed most frequently in human monocytes. The CDNA of each gene has a sequence fully defined in the specification, and lacking the CAYG sequence located adjacent to polyA region. Also described are: (1) an antibody considered to consider the protein encoded by any of the genes; (2) colliquoudleotides obtained from the CDNA sequences; (3) 380 human genes which are expressed most frequently in human macrophages; differentiated from human monocytes by granulocyte-macrophage colony-stimulating factor, the CDNA of each gene has a fully defined sequence, given in the specification, lacking the base sequence CATG located most closely to the specification, lacking the base sequence CATG located most closely to the poly A region; (4) an antibody specifically for the protein encoded by carry of the genes of (3). The genes and CDNAs, are used for the study of gene specificity and disease onset mechanism e.g. oncogenesis, genetic diseases, drug development and diagnosis. AAASSGIOT to AAASSGESE represent
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                                                                                                                                                                                                                                                                                                                                                                      Genes most frequently expressed in human monocytes and GM-macrophages and M-macrophages studied and with cDNAs characterized, for study of gene specificity, disease onset mechanism, drug development and diagnosis.
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                                                       Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag; granulocyte-macrophage colony-stimulating factor; characterisation; GM-CSF; identification; diagnosis; gene specificity; oncogenesis; disease onset mechanism; genetic disease; drug development; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
granulocyte-macrophage colony-stimulating factor; characterisation;
GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifically claimed oligonucleotide tag sequences for human genes
                             Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 1 A; 7 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               Suzuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed in monocytes and macrophages
                                                                                                                                                                                                                                                                                (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 31; Page 115; 138pp; Japanese.
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(first entry)
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Best Local Similarity
                                                                                                                                                            WO200024892-A1.
                                                                                                                                 Homo sapiens.
07-SEP-2000
                                                                                                                                                                                                                                                                                                             Hashimoto S,
                                                                                                                                                                                                                       28-OCT-1999;
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                                                                                                                                                                                           04-MAY-2000
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(first entry)

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The present invention describes 100 human genes, which are expressed most frequently in human monocytes. The CDNA of each gene has a sequence fully defined in the specification, and lacking the CATG sequence located adjacent to polyA region. Also described are: (1) an antibody specifically for the protein encoded by any of the genes; (2) oligonucleotides obtained from the CDNA sequences; (3) 380 human genes which are expressed most frequently in human macrophages, differentiated from human monocytes by granulocyte-macrophage colony-stimulating factor, the CDNA of each gene has a fully defined sequence, given in the construction of the genes of (3), and (5) oligonucleotides obtained from the cDNA cany of the genes of (3), and (5) oligonucleotides obtained from the cDNA sequences of (3). The genes and cDNAs, are used for the study of gene specificity and disease onset mechanism e.g. oncogenesis, genetic diseases, drug development and diagnosis. AAAAS6107 to AAAAS6586 represent expressed in monocytes and macrophages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes most frequently expressed in human monocytes and GM-macrophages M-macrophages studied and with cDNAs characterized, for study of gene specificity, disease onset mechanism, drug development and diagnosis.
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disease onset mechanism; genetic disease; drug development; ss.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 43; Page 127; 138pp; Japanese.
                                                                                                                                                                                                                                                                                   99WO-JP005982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsushima K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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                                                                                                                                         WO200024892-A1
                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                   28-OCT-1999;
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RESULT 372
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                                                                                                                                                                                                                                                                                                                                                                           The present invention describes 100 human genes, which are expressed most frequently in human monocytes. The cDNA of each gene has a sequence fully defined in the specification, and lacking the CATG sequence located adjacent to polyA region. Also described are: (1) an antibody capecifically for the protein encoded by any of the genes; (2) oligonucleotides obtained from the cDNA sequences; (3) 380 human genes which are expressed most frequently in human macrophase, differentiated comman monocytes by granulocyte-macrophage colony-stimulating factor, the cDNA of each gene has fully defined sequence, given in the specification, lacking the base sequence CATG located most closely to the specification; (4) and mantbody specifically for the protein encoded by any of the genes of (3), and (5) oligonucleotides obtained from the cDNA sequences of (3). The genes and cDNAs, are used for the study of gene specificity and disease onset mechanism e.g. oncogenesis, genetic specifically claimed oligonucleotide tag sequences for human genes cypressed in monocytes and macrophages
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                                                                                                                                                                                                                                                  Genes most frequently expressed in human monocytes and GM-macrophages and M-macrophages studied and with cDNAs characterized, for study of gene
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                                                                                                                                                                                                                                                                                                  specificity, disease onset mechanism, drug development and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 1 A; 7 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                          Hashimoto S, Matsushima K, Suzuki T;
                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 102; 138pp; Japanese.
                                                                                                             (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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98US-0089844P.
98US-0089853P.
98US-0089878P.
                   99WO-JP005982
                                                                98JP-00307532
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                   28-OCT-1999;
                                                                28-OCT-1998;
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Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts which are expression) tags used to identify mRNA transcripts which are differentially expressed in a variety of normal or malignant cell types. Some of the transcripts correspond to known genes or ESTS (expressed conference tags) which were previously unknown to be preferentially or differentially expressed in that particular cell type, while other transcripts correspond to novel genes. The invention also provides a nucleotide comprising a promoter sequence derived from one of the conference comprising the polymucleotides of the invention. A nucleotide comprising the polymucleotides of the invention. A nucleotide comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures to characterise a cell of a specific tissue type and to determine whether cell is normal or malignant. They may be used to determine whether the is a normal or malignant. They may be used to screen for agence that modulate expression of differentially expressed genes compound. The promoter/foreign gene construct of the invention may be used for targetted expression of the foreign gene in a particular cell type. For example, a promoter derived from a gene preferentially expressed in dendritic cells (antigen-presenting cells, or APCs), may be operably linked to a sequence encoding an immunostimularory molecule and a sequence encoding an antigen. Such a construct could be transduced into a sequence encoding an immunostimularory molecule and a construct could be transduced into a manume effector cells in vivo, or in cancer immunotherapy
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                                                                                                                                            98US-0090036P.
98US-0090039P.
98US-0090040P.
98US-0090041P.
98US-0090042P.
                        98US-0089997P.
98US-0089999P.
98US-0090000P.
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98US-0090077P.
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Best Local Similarity
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19-JUN-1998;
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                                                                       SAGE tag; serial analysis of gene expression; diagnosis; differential gene expression; characterisation; targetted expression; tumour; cancer; immunotherapy; ss.
                                                       Human prostate preferentially expressed gene SAGE tag, SEQ ID NO:101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 57; 97pp; English.
                                                                                                                                                                       98US-0089833P.
98US-0089842P.
98US-0089932P.
98US-0089932P.
98US-0089932P.
98US-0089932P.
98US-0089932P.
98US-0089932P.
98US-0099032P.
98US-0090035P.
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       AAZ79810 standard; DNA; 10 BP
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                                       10-APR-2000 (first entry)
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ROBERTS B L.
SHANKARA S.
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AAZ79810/c
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cells comprising the polynucleotides of the invention. A nucleotide comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures to characterise a cell of a specific tissue type and to determine whether it is normal or malignant. They may be used to screen for agents that modulate expression of differentially expressed genes compound. The promoter/foreign gene construct of the invention may be used for targetted expression of the foreign gene in a particular cell type. For example, a promoter derived from a gene preferentially expressed in dendritic cells (antigen-presenting cells, or APCs), may be operably linked to a sequence encoding an immunostimulatory molecule and a sequence encoding an antigen. Such a construct could be transduced into APCs and would be useful for inducing an immune response by educating immune effector cells in vivo, or in cancer immunotherapy
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98US-0089844P
98US-0089813P
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Query Match
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                                                                                                                                                                                                   expression) tags used to identify mRNA transcripts which are differentially expressed in a variety of normal or malignant cell types. differentially expressed in a variety of normal or malignant cell types. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in that particular cell type, while other transcripts correspond to novel genes. The invention also provides a nucleotide comprising a promoter sequence derived from one of the conformation approaches degenes, which may optionally be operably linked to a foreign nucleotide sequence, and gene delivery vehicles and host cells comprising the polynucleotides of the invention. A nucleotide comprising sequences AAZ79110-Z79916 may be used in diagnostic procedures to characterise a cell of a specific tissue type and to determine whether it is normal or malignant. They may be used to screen for agents that modulate expression of differentially expressed genes compound. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
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                                                                                                                                                      New polynucleotide useful in cancer immunotherapy
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98US-0090079P.
98US-0090080P.
98US-0111715P.
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                                                                                                   Shankara S;
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                                                 (GENZ ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                                                                             WPI; 2000-106132/09
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Best Local Similarity
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                                                                                                                                                                                New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular
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pred. No. 2.5e+02;
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                                                                 Kinzler KW;
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Velculescu VE,
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cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                                                                                                         Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
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                                                                      Human ubiquitously expressed transcriptome sequence SEQ ID NO: 874
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                                                                                                                                     The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                    transient receptor potential family; BWS; Beckwith-Wiedemann syndrome; 11p15.5 abnormality; chromosome 11; anticancer; developmental activity; intracellular calcium ion regulation; hormone; growth factor; apoptosis; cell growth; cell death; cell differentiation; urogenital disease; polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
                                                                             New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular
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                                       Kinzler KW
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                                                                                                                    Claim 13; Page 64; 94pp; English.
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                                       Vogelstein B,
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99US-00448480
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This invention describes a novel DNA sequence (I) encoding the WTR1 crotein that: (i) has at least one biological activity of a TRP cream that: (i) has at least one biological activity of a TRP creaming the receptor potential) family procein, (ii) is connected with tumors involving Ilp15.5 abnormalities. The products of the with tumors involving Ilp15.5 abnormalities. The products of the invention have anticancer and developmental activity. MRT1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases, including polycystic kidney disease. (I) and related ribozymes, antisense CR NNA, proteins and antibodies (Ab) are used to treat or prevent diseases consociated with altered expression of the MRT1 gene or activity of its protein, or with calcium influx into cells, e.g. BWS, Wilms tumor, rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (I) can also be used for recombinant production of MRT1 proteins (II) (used for analysis, characterization and therack and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for biochips, and to raise anti-protein or competitive assays for (II), as tissue markers, for identifying competitive assays for (II), as tissue markers, for identifying competitive assays for (II) are used to raise Ab, as reagents in competitive assays for (II) are used to raise Ab, as reagents in the proceins and in screening for (ant) agonists. This sequence contributed in creening for (ant) adonises in the proceins in the proceins and in screening for (ant) adonises. This sequence in the proceins and in screening for (ant) adonises in the proceins in the proceins and in screening for gase and related sequence of punction region described in the purchase of the punction of 
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DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies.
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Pred. No. 2.5e+02;
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                                                                                                                                                            Example 2; Fig 2; 46pp; German.
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Claim 10; Page 20; 52pp; Japanese.

The present invention describes an lipopolysaccharide (LPS) activated human monocyte expression gene group consisting of the high-ranking 50 genes of the highest expression among the genes expressed by human monocyte stimulated by LPS in which the cDNR of each gene has the base sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-CATG-3' nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treatment of various human diseases in which human monocyte plays an important role. AAH32628 to AAH32943 represent specifically claimed LPS activated human monocyte expression gene cDNA tags from the present invention. AAH33294 represents an LPS activated human monocyte expression gene cDNA sequence encoding AAB98009, which are given in the exemplification of the present invention

Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90...
Best Local 9; Conservative 10 CGCCCCTTCC 19 ઠે

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AAF70452 standard; DNA; 10 BP. RESULT 381 AAF70452/c

(first entry) 20-APR-2001 AAF70452;

Human DRD2 polymorphism detection oligonucleotide primer SEQ ID NO:195 Human, dopamine receptor D2, DRD2, polymorphism; allele specific, drug target isogene, detection, single nucleotide polymorphism; SNP, genotype, schizophrenia, Parkinson's disease, myoclonus dystonia; MD; probe; PCR primer; ss.

Homo sapiens

WO200105832-A1.

25-JAN-2001,

19-JUL-2000; 2000WO-US019644.

99US-0144493P. 19-JUL-1999;

(GENA-) GENAISSANCE PHARM INC.

Stephens JC; Duda A, Nandabalan K, Denton RR, Chew A,

WPI; 2001-091967/10.

Polynucleotides comprising single nucleotide polymorphisms in the human dopamine receptor D2, useful for detecting mutations associated with, e.g. schizophrenia, Parkinson's and myoclonus dystonia.

Disclosure; Page 25; 135pp; English.

The present invention describes polynucleotides comprising single nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2). The polynucleotides may be used in assays to detect and characterise polymorphisms in DRD2 that affect its expression and activity and are involved in disorders such as schizophrenia, Parkinson's and myoclonus dystonia (MD). This information would be useful for studying the biological function of BND2 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. Polymorphisms in the DRD2 gene affect the expression of active and functional polypeptides. Therefore it is

advantageous to detect polymorphisms in the DRD2 gene and how those polymorphisms are combined in different copies of the gene. AAF70261 to AAF70308 represent human DRD2 allele specific oligonucleotide probes, and AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide primers which are used in the detection of DRD2 polymorphisms. AAF70405 represent oligonucleotide primers for the detection of human DRD2 polymorphisms which are given in the exemplification of the present invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2 gene which are used in examples from the present invention

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Sequence 10 BP; 3 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Gaps ö 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0%,
Conservative

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TCCTAAGCAT 26 ||||||| ||| TCCTAACCAT 1 17 10 ઠે g

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Gaps

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RESULT 382 ABA83151/c

ABA83151 standard; cDNA; 10 BP.

ABA83151;

(first entry) 08-FEB-2002

Glutathione peroxidase 3 ovarian tumour marker gene SAGE tag, #111.

Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; mucinous cystadenoma; aleancer cell adenocarcinoma; adenocarcinoma; adenocarcinoma; adenocarcinoma; cystadenoma; adenocarcinoma; engane carcinoma; adenocibroma; Brenner tumour; serial analysis of gene expression; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine; SAGE tag; ss

Homo sapiens.

WO200175177-A2.

11-OCT-2001.

03-APR-2001; 2001WO-US010947.

03-APR-2000; 2000US-0194336P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Sherman-Baust CA, Pizer ES, Hough CD;

WPI; 2001-626450/72.

Morin PJ,

Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker gene.

Claim 26; Page 41; 140pp; English.

The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83181-ABA83182, ABA83189, ABA83181 or segments thereof (ABA83123-ABA83186, ABA83189, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for

monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an apithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, mucinous cystadenoma, borderline serous tumour, mucinous ovarian tumour, edear carcinoma, cystadenocarcinoma, cystadenocarcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, archardibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prevention of ovarian cancer. Sequences ABA83123-ABA83169, ABA83179, ABA83181 and ABA83183 represent SAGE tags derived from the ovarian tumour monitoring a patient in remission from ovarian cancer and in tests for prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treament and marker genes of the invention

Sequence 10 BP; 2 A; 1 C; 7 G; 0 T; 0 U; 0 Other;

Gaps ; 0 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels 9; Conservative Query Match Best Local Similarity Matches 9; Conserv

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11 GCCCCTTCCT 20 Н 10 deceerreer ð

RESULT 383

AAF33574 standard; DNA; 10 BP. AAF33574; Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:313.

(first entry)

23-MAR-2001

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000

14-JUN-2000; 2000WO-US016223

16-JUN-1999;

99US-00335032

(UYJO) UNIV JOHNS HOPKINS.

Kinzler Vogelstein B, WPI; 2001-061874/07. Jelculescu V,

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Claim 1; Page 386; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated OMF) genes comprising a SAGE (serial analysis of gene expression) tag. Also

described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cleast 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNR with a probe which comprises at least 10 comprision mucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and contitoring expression in the yeast cell of at least 1 NORF genes whose expression is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle cycle and for identification of antifungal drugs. AAF33268 to AAF44064 crepresent SAGE tags used in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Gaps 0; 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; 1; Indels 0; Mismatches 9; Conservative Local Similarity Query Match Matches

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11 GCCCCTTCCT 20 10 1 GACCCTTCCT ò 움

AAF33874/C

AAF33874 standard; DNA; 10 BP. AAF33874;

(first entry) 23-MAR-2001 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:613.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032. 16-JUN-1999;

SNIXAOH SNHOC AINO (OCKI)

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Claim 1; Page 397; 419pp; English

The present invention describes an isolated DNA molecule comprising a Example; Page 65; 419pp; English.

CC coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORP) genes CC comprising a SAGE (serial analysis of gene expression) tag, Also Gescribed are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at Cast Inf) between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for contriguous nucleotides of a NORF gene whose expression of dentifying human DNA with a probe which comprises at least 10 contriguous nucleotides of a NORP gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell of at least 1 NORP gene whose expression is affected by the class of drugs. The NORF genes may be used to set of identify andidate drugs which a ffect the cell cycle. The methods may be used as markers of phases of the cell cycle. The cettoresent SAGE tags used in the exemplification of the present invention. APRF31267 represent linkers and PCR primers used in the second in the avanned; in the avanned in the avanned in the savenned in the avanned in the savenned in the avanned in the avanced method, in the exemplification of the present invention \$

Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

; 0 Query Match 32.3%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels 4 CCTCATCGCC 13 ò

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10 CCTCATCACC 1

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AAF35101 standard; DNA; 10 BP AAF35101; RESULT 385

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1840.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle, NORF; nor previously assigned open reading frame; nonamnotated ORF; SAGE; Berial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

SNING ONIV JOHNS HOPKINS

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cycle comprising administering a NORF gene whose expression varies by at charge comprising administering a NORF gene whose expression of phase, S phase and (2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a candidate drug as a member of a comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and constructing expression in the yeast cell of at least 1 NORF gene whose cycressed genes may be used as markers of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The control cycle and fetct phases of the cell cycle, the differentially cycle and for identification of antifungal drugs. AAF33268 to AAF44064

Cycle and for identification of antifungal drugs. AAF3368 to AAF44064

Cycle and for identification of antifungal drugs. AAF3368 to AAF44064

Cycle and for identification of antifungal drugs. AAF3368 to AAF44064
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AAF35078 standard; DNA; 10 AAF35078; RESULT 386

BP.

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1817.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification, linker, PCR primer, ds.

Saccharomyces cerevisiae,

WO200077214-A2

21-DEC-2000.

14-JUN-2000; 2000WO-US016223,

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS.

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of

Kinzler K;

Vogelstein B,

Velculescu V,

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate continual drugs comprising: (a) contexting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a continuous nucleotides of a NORF gene whose expression is affected by the class of drugs. The NORF gene may be used conspicion of a contiguous nucleotides as markers of phases of the cell cycle. The contiguous mucleoting expression in the yeast cell with a candidate drug and contacting a yeast cell with a method whose expression is affected by the class of drugs. The NORF gene may be used to identify candidate drugs which affect the cell cycle and feet phases of the cell cycle the cell cycle and effect phases of the cell cycle the cell cycle and feet phases of the cell cycle and feet dentify candidate drugs which affect the cell cycle and feet phases of the cell cycle and feet dentify candidate drugs which affect the cell cycle and feet phases used in the exemplification of the present invention the present invention of the present inv
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gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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Pred. No. 2.5e+02;
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                                                                    Example; Page 64; 419pp; English.
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises in the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human DNA with a probe which comprises in INI; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF genes whose cypeasion is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. ABF3326 to AAF44064 crepresent SAGE tags used in the exemplification of the present invention. ö Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Gaps Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. ö 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels method, in the exemplification of the present invention Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:314. Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other; Example; Page 108; 419pp; English AAF33575 standard; DNA; 10 BP. 14-JUN-2000; 2000WO-US016223. 99US-00335032 SNIX4OH SNHOL VINU (OLYU) 23-MAR-2001 (first entry) 9; Conservative Saccharomyces cerevisiae. 8 ATCGCCCCTT 17 1 ATCGCCGCTT 10 WPI; 2001-061874/07. Query Match Best Local Similarity WO200077214-A2. 16-JUN-1999; 21-DEC-2000. AAF33575; RESULT 388 Matches AAF3357 ઠે 엄

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle sclose and (2/M; (2) a method (M2) for screening candidate bhase of the cell cycle sclose and (2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contribution buman DNA with a probe which comprises at least 10 contributions nucleotides of a NORF gene whose expression of a NORF gene whose expression in a contiguous nucleotides of a NORP gene whose expression in a contiguous nucleotides of a NORP gene whose expression in a cyeast cell comprising contacting a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug as a member of a cyeast cell comprising contacting a yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to sentification of drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention.
                                                                                                                Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                        Velculescu V, Vogelstein B, Kinzler K;
                                                                                                                                                                                                               Claim 1; Page 386; 419pp; English.
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Matches 9; Conservative
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                                                                      WPI; 2001-061874/07.
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AAF33573
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Gaps

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle salected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting a probe which comprises at least 10 contiguous nucleotides of a NORP gene whose expression nucleotides of a NORP gene whose expression in a contiguous nucleotides of a NORP gene whose expression in a cyeast cell of at least 1 NORF gene whose contiguous nucleotides of a NORP gene whose expression in the yeast cell of at least 1 NORF gene whose cyeast cell comprising contacting a yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene whose cyeast cell comprising contacting a yeast cell of at least 1 the cile of the strugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs which affect the cell cycle and cycle and for identification of antifungal drugs and the present invention.

Cycle and for identification of the present invention.

Cycle and characte
                                                                                                                                                                                  Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                              Kinzler K;
                                                                                                                                                                                                                                                                                Claim 1; Page 386; 419pp; English.
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                                                                                         Velculescu V, Vogelstein B,
  99US-00335032
                                             (UYJO ) UNIV JOHNS HOPKINS.
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16-JUN-1999;
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cantifungal drug; comprising: (a) contexting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying whose expression varies as in M1; and (4) a method (M4) for identifying a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contioning expression in the yeast cell of at least 1 NORF gene whose contidion may be used as markers of phases of the cell cycle. The expression is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF43367 represent linkers and PCR primers used in the exemplification of the present invention.
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                                                                                                                                                                                                                                Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                Kinzler K;
                                                                                                                                                                                                                                                                                                                     Example; Page 46; 419pp; English.
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                                                                                                                                                Vogelstein B,
                   14-JUN-2000; 2000WO-US016223
                                                             99US-00335032
                                                                                                       (UYJO ) UNIV JOHNS HOPKINS
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Matches 9; Conservative
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                                                             16-JUN-1999;
                                                                                                                                                Velculescu V,
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamontated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cutifungal drugs comprising: (a) contacting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying the probe which comprises at least 10 comprising contacting human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; cand (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a class of drugs. The NORF genes may be used continuous mucleotides of a NORF gene whose cycle and for identification of an early monitor and affect phases of the cell cycle, the differentially cexpression is affected by the class of drugs. The NORF genes may be used to identification of an early monitor and affect phases of the cell cycle cycle and for identification of an early whose cycle and for identification of an early monitor in the exemplification of the present invention.

Cycle and for identification of an early primers used in the SAGE method, in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                   Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                                  Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 127; 419pp; English
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                                                                                          14-JUN-2000; 2000WO-US016223.
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WO200077214-A2
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14-JUN-2000; 2000WO-US016223.
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                                  99US-00335032
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90.0%;
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                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                     ccrrccrarg 10
                                                         WPI; 2001-061874/07.
                                                                                                                                                                                                             Query Match
Best Local Similarity
           WO200077214-A2.
                                  16-JUN-1999;
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                   21-DEC-2000
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Isolated polymorphic variants of chemokine (C-C motif) receptor 3 (CCR3) gene useful for studying function of CCR3, expressing the CCR3 protein and to screen drugs to treat CCR3 activity-related diseases. Claim 18; Page 13; 53pp; English. 1 CCACCTCATC 10 polymorphisms Homo sapiens. Best Loc Matches RESULT 394 AAD25442/ g ð The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes coding sequence of a yeast gene selected from page 18 ABGE (serial analysis of gene expression) tag. ABGO described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate of antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contiguous nucleotides of a contiguous nucleotides of a NORF gene whose expression of contiguous nucleotides of a NORF gene whose expression varies as in M1; and (b) muman genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cyeast cell comprising conteacting a yeast cell with a candidate drug and yeast cell comprising conteacting a yeast cell with a candidate drug and cyeast cell comprising conteacting a yeast cell with a candidate drug and conteacting a yeast cell of at least 1 NORF gene whose expressed genes may be used to darnot the vests of phases of the cell cycle. The cycle and for identification of antifungal drugs which affect the coll cycle and for identification of antifungal drugs. AAF33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention. ö Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Gaps ö Score 8.4; DB 1; Length 10; Pred. No. 2.5e+02; 1; Indels Human CCR3 gene polymorphism detecting primer #6. Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other; 0; Mismatches Kinzler K; Example; Page 278; 419pp; English. AAD25240 standard; DNA; 10 BP. Saccharomyces cerevisiae.

Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;

genotyping, type IV hypersensitivity reaction, HIV-1, gene therapy, human immunodeficiency virus 1; polymorphism; primer; ss. (GENA-) GENAISSANCE PHARM INC. 18-MAY-2001; 2001WO-US016278. 18-MAY-2000; 2000US-0205191P. Koshy B; WPI; 2002-055681/07. Choi JY, Kazemi A, WO200187908-A2 Homo sapiens. 22-NOV-2001

The invention relates to genetic variants of human chemokine (C-C motif)
receptor 3 (CCR3) gene. The invention also relates to compositions and
methods for hablotyping and/or genotyping the CCR3 gene in an individual.
CCC methods for the invention are useful for studying the expression
and function of CCR3 and in expressing CCR3 proteins for use in screening
candidate drugs to treat diseases related to CCR3 activity. They are also
used in gene therapy. The polymorphism and haplotype data is useful for
validating whether CCR3 is a suitable target for drugs to treat type IV
hypersensitivity reactions and human immunodeficiency virus (HIV)-1,
CCC screening for such drugs and reducing bias cells in clinical trials of
such drugs. The genotyping method is useful for determining whether an
individual has one haplotype or haplotype pairs. The haplotyping method
is useful for improving the efficiency and outcome of several steps in
the present sequence is a primer used for detecting human CCR3 gene

Gaps ö .Match 32.3%; Score 8.4; DB 1; Length 10; Local Similarity 90.0%; Pred. No. 2.5e+02; es 9; Conservative 0; Mismatches 1; Indels Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other; Query Match

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踞. AAD25442 standard; DNA; 10 (first entry) 1 ccacgrcarc 10 12-MAR-2002 AAD25442;

Human; gonadotropin-releasing hormone 2; GNRH2 gene; haplotyping; genotyping; gene therapy; reproductive disorder; polymorphism; primer; Human GNRH2 gene polymorphism detecting primer #13.

WO200187910-A2. 22-NOV-2001

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WPI; 2002-130787/17.
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                                                                                                                                                                                                 The invention relates to genetic variants of human gonadotropincreleasing hormone 2 (GNRH2) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the GNRH2 gene in an individual. Polymucleotides of the invention are useful for studying the expression and function of GNRH2 and in expressing GNRH2 proteins for use in screening candidate drugs to treat diseases related to GNRH2 activity. They are also used in gene therapy. The methods of the invention are useful in determining whether an individual has a haplotype or haplotype pairs. The haplotyping method is useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with GNRH2 activity, e.g., reproductive disorders. The present sequence is a primer
                                                                                                                              New genetic variants of gonadotropin-releasing hormone 2 isogene, useful in studying expression and function of protein and for screening drugs to treat diseases e.g. reproduction disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNE; chromosome 17p13-12; acetylcholine receptor; AChR; neuromuscular junction; skeletal muscle; postnatal development; congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype; genetic variant; single nucleocide polymorphism; SNP; gene therapy; drug screening; primer extension; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                  32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                       activity, e.g., reproductive disorders. The presenused for detecting human GNRH2 gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                  Sausker EA;
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                                                                                  Nandabalan K,
                                                                                                                                                                             Claim 18; Page 13; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL88346 standard; DNA; 10 BP.
                                                          PHARM INC
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           18-MAY-2001; 2001WO-US016353
                                 18-MAY-2000; 2000US-0205187P
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                14 CCTTCCTAAG 23
                                                         (GENA-) GENAISSANCE
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                                                                                 Duda A,
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The invention relates to a method for haplotyping the cholinergic receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an individual, and also describes 17 novel polymorphic sites within the human CHRNE gene. The CHRNE pene is located on chromosome 17p13-12 and contains 12 exons which encode a 493 amino acid protein (ABB49112). The CHRNE protein is one of the 5 subunits of mammalian acetylcholine creeptors (AChRs) found at neuromuscular junctions in juveniles and adults, and is essential for the normal postnatal development of skeletal muscle. Mutations in the CHRNE gene ere associated with congenital creeptors (AChRs) found at neuromuscular junctions in juveniles and adults, and is essential for the normal postnatal development of skeletal consistence (CMS). CHRNE gene sequences can therefore be used in mysathenic syndrome (CMS). CHRNE gene sequences can therefore be used in conformation of CHRNE, and in expressing CHRNE protein for use in conformation of CHRNE, and in expressing CHRNE protein for use in an individual, and can also be used in pharmaceutical research to validate condidate drugs for, treating a specific condition drugs or disease condidate drugs for, treating a specific condition drugs or disease condidate drugs for, treating a specific condition drugs or disease configuration using oligonucleotide primers comprising sequences the target region may be determined by the use of allele-specific oligonucleotides (ASOS; ABL88370-ABL88320) as probes and primers, and by primers and reliability of several steps in the discovery and efficiency and reliability of several steps in the discovery and chalsables for treating diseases associated with CHRNE sequences the value of activity, and may be used to screen drugs which target CHRNE sequences the prediction by reliance to the primers used to detect polymorphisms in the CHRNE gene by
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Novel genetic variants of cholinergic receptor, nicotinic, epsilon by golypeptide gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. congential myasthenic syndrome.
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                                                                                                                                                                                                                                           English
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                                                                                                                                                                                                                                 Claim 19; Page 15; 104pp;
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The invention comprises the amino acid and coding sequence of the human interleukin 12A (IL-12A) protein. Specifically the invention relates to the identification of polymorphisms within the human (IL-12A) gene sequence. The polymorphisms identified in the human IL-12A gene sequence are useful in studying the expression and function of IL-12A, and in tuberculosis for the treatment of disorders such as AIDS, malaria, tuberculosis and cancer. The IL-12A polymorphisms may be used to haplotype and genotype the IL-12A gene of an individual. The IL-12 DNA studying expression of the IL-12A gene of an individual. The IL-12 DNA studying expression of the IL-12A isogenes in vivo. The present DNA sequence represents a human interleukin 12A (IL-12A) gene primer
                                                                                                                                                                                                    New interleukin 12A (IL-12A) gene polymorphic variants, for studying expression and function of IL-12A and screening candidate drugs for treating AIDS and cancer.
        Kliem SE,
        Gilson CR,
    Choi JY,
                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 13; 72pp; English.
    Cappola G,
                                                                                                                     WPI; 2002-315865/35.
Armstrong B,
Parks KE;
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the

Koshy

Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

ö 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels Local Similarity 90.0 nes 9; Conservative Query Match Best Loc Matches

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Gaps

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ABA98377 standard; DNA; 10 BP. ABA98377/

30-JUL-2002 (first entry) ABA98377; CCXSXLLLLXSXLXBXBXBXBXSXXXXXXBXBXCXX

SCN2B gene polymorphisms oligonucleotide primer #3.

Human; sodium channel voltage gated type 2 beta polypeptide; SCN2B; ds; gene therapy; neuroprotective; demyelinating disease.

Homo sapiens

25-OCT-2001.

03-APR-2001; 2001WO-US010743.

13-APR-2000; 2000US-0196597P.

(GENA-) GENAISSANCE PHARM INC

Choi JY, Koshy B;

Chew A,

WPI; 2002-075072/10.

New polynucleotide containing polymorphisms in the human sodium channel voltage gated type 2 beta polypeptide (SCN2B) gene, for developing drugs for treating demyelinating diseases.

This invention relates to an isolated polynucleotide which is a polymorphic variant of a reference sequence for sodium channel voltage Claim 17; Page 13; 63pp; English.

gated type 2 beta polypeptide (SCNZB) gene. The methods have applicability in developing diagnostic tests and therapeutic treatments for demyelinating diseases. The protein is useful for studying the expression and function of SCNZB and expressing SCNZB protein for use in screening for candidate drugs to treat diseases related to SCNZB contribly. The polymorphism and haplotype data are useful for validating whether SCNZB is a suitable target for drugs to treat demyelinating chasases, screening for such drugs and reducing bias in clinical trials. The haplotyping method is useful to validate SCNZB as a candidate target for treating a specific condition or disease predicted to be associated with SCNZB activity. A recombinant non-human organism transformed or transfected with the polypeptide is useful for studying expression of the SCNZB isogenes in vivo, for in vivo screening and testing of drugs and compounds for demyelinating diseases in a biological system. This sequence is used during the detection of polymorphisms of the SCNZB gene ö New genetic variants of Homeo Box D3 for studying expression and function of the protein, and for screening drugs to treat diseases e.g. developmental disorders and tumors. The invention relates to genetic variants of the homeo box D3 (HOXD3) gene. HOXD3 gene includes 9 polymorphic sites PS1-PS9. Haplotypes (HTS) or haplotype pairs (HP) for PS1-PS9 in the HOXD3 gene are useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with HOXD3 activity, e.g., developmental disorders and tumours. HOXD3 isogene is useful in studying the expression and function of HOXD3 and in expressing HOXD3 protein for use in screening for candidate drugs to treat diseases related to HOXD3 activity and in studying the effect of Human, homeo box D3; HOXD3; polymorphism; developmental disorder; haplotype; HT; allele-specific oligonucleotide; ASO; tumour; therapy; drug screening; cytostatic; primer; 88. Gaps Human homeo box D3 (HOXD3) gene polymorphism detecting primer #14. ö 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other; Koshy B, Kumar AM; Claim 18; Page 13; 66pp; English. AAD25215 standard; DNA; 10 BP. (GENA-) GENAISSANCE PHARM INC. 24-MAY-2001; 2001WO-US016982 25-MAY-2000; 2000US-0207076P Query Match Best Local Similarity 90.0°, Best Acal 9; Conservative (first entry) 11 GCCCCTTCCT 20 WPI; 2002-075363/10. Kazemi A, WO200190127-A2 Homo sapiens. 12-MAR-2002 29-NOV-2001. 10 AAD25215; Duda A, RESULT 398 AAD25215 \$ ઠ 유

e.g. cataract. and can also be used by the

the introduction retailed to a reference sequence for crystallin, beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment, where the polymorphic variant comprises a CRYBB1 isogene defined by a chaptotype from haplotypes 1-16 as given in the specification. Also included are a transgenic non-human animal transformed or transfected with the polymorphic variant, a computer system for storing and analysing colymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene which comprises the defined CRYBB1 isogenes, methods of determining an individuals haplotype or genotype as well as methods of determining the sesociation of a particular haplotype with a disease or trait and a composition comprising at least one genotyping oligonucleotide (specially allele-specific oligonucleotides (ASO)) for detecting a composition comprising at least one genotyping oligonucleotide for polymorphism in the CRYBB1. The isogenes or haplotypes are useful for improving the efficiency and reliability of several steps in the improving the efficiency and reliability of several steps in the ö The invention relates to an isolated polynucleotide comprising a sequence the variation on the biological activity of HOXD3 as well as on the binding affilinty of candidate drugs targeting HOXD3 for the treatment of developmental disorders and tumours. An antibody against HOXD3 is useful in a variety of diagnostic and prognostic formats and therapeutic Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmalogical; cataract; allele specific oligonucleotide; ASO; ss; haplotype; genotyping; transgenic animal; PCR primer; primer extension. assaying Novel polymorphic variants of crystallin, beta Bl useful in studying expression and function of the protein, useful for screening candidate drugs to treat diseases e.g. cataract. methods. A recombinant non-human organism is useful in studying expression of the NOXD3 isogenes in vivo. Allele-specific oligonuclectides (ASO) are useful as probes and primers and for assay: a polymorphism in the target region. The present sequence is a primer Gaps ; 0 Human CRYBB1 gene ASO primer extension PCR primer 3' end #21. 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; 1; Indels Rounds E; used for detecting human HOXD3 gene polymorphisms Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other; 0; Mismatches Koshy B, Claim 17; Page 13; 94pp; English. Kazemi A, Kliem SE, AAS97362 standard; DNA; 10 BP. (GENA-) GENAISSANCE PHARM INC 05-MAY-2000; 2000US-0202253P. 07-MAY-2001; 2001WO-US014715. (first entry) Local Similarity 90.0 5 CTCATCGCCC 14 10 CTCAGCGCCC 1 WPI; 2002-062253/08. WO200185998-A1. Homo sapiens. 12-MAR-2002 15-NOV-2001 Choi JY, AAS97362; Query Match Best Loc Matches RESULT 399 888888888888888 셤 ઠ

ö pharmaceutical research scientist to validate CRYBB1 as a candidate target for, and in design of clinical trials of candidate drugs for, treating a specific condition drugs or disease predicted to be associated with CRYBB1 activity. The ASOs are useful as probes and primers, and for assaying a polymorphism in the target region. The present sequence is the allele specific 3' end of a PCR primer used in primer extension experiment to detect polymorphisms in CRYBB1 The invention comprises the human lysosomal acid phosphatase 2 (ACP2) nucleic acid and protein sequences. Specifically, the invention relates to the discovery of 22 novel polymorphic sites within the APC2 gene. The invention also comprises methods for haplotyping and genotyping the ACP2 gene in an individual. The ACP2 gene (located on chromosome 11) encodes a lysosomal-specific enzyme that catalyses the hydrolysis of orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and protein are pharmaceutically important in the treatment of Hodgkin's protein are pharmaceutically important in the treatment of Hodgkin's polymorphisms of the invention are useful in haplotyping the ACP2 gene. ACP2 haplotyping is useful in validating ACP2 as a target (and designing divise) for treating an ACP2-related disease or condition (e.g. Hodgkin's disease and acid phosphatase deficiency. The ACP2 gene polymorphisms are useful for ACP2 genotyping, which can also be used to develop diagnostic Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11; lysosome-specific enzyme; orthophosphoric monoester hydrolysis; Hodgkin's disease; HD; acid phosphatase deficiency; novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism; transgenic animal; pirimer; probe; primer-extension oligonucleotide; SNP; single nucleotide polymorphism. Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. Hodgkin's disease. Gaps Human lysosomal acid phosphatase 2 primer-extension oligonucleotide ö 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; rive 0; Mismatches 1; Indels Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other; Claim 19; Page 15; 109pp; English. Tanguay DA; ABL36365 standard; DNA; 10 BP. (GENA-) GENAISSANCE PHARM INC. 07-JUN-2001; 2001WO-US018457. 07-JUN-2000; 2000US-0210047P. 22-APR-2002 (first entry) 9; Conservative 7 CATCGCCCCT 16 CATGGCCCCT 10 Меввег С, WPI; 2002-154563/20. Best Local Similarity WO200194362-A2 Homo sapiens. 13-DEC-2001. Kliem SE, ABL36365; Query Match Matches 8888888888 ò 셤

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which is a polymorphic variant of a reference sequence for the human smoothened brosophila homologue (SMOH) gene or its fragment, or a smoothened brosophila homologue (SMOH) gene or its fragment, or a polymorphic variant of a reference sequence for a SMOH CDNA or its fragment. A new isolated polypeptide is useful for screening for drugs targeting the polypeptide. A new method is useful for identifying an association between a trait such as a clinical response to a drug targeting SMOH and a haplotype or haplotype pair of SMOH gene. The methods have applicability in developing diagnostic tests and therapeutic reatments for basal cell carctinomas (BCCs). The isolated polymucleotide is useful for studying the expression and function of SMOH and expressing SMOH protein for use in screening for candidate drugs to treat diseases related to SMOH activity. The polymorphism and haplotype data are useful for validating whether SMOH is a suitable target for drugs to treat BCCs, creening for the drugs and reducing bias in clinical trials of the drugs. The isolated polymucleotide is useful for therapeutic purposes.
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tests and therapeutic treatments. The ACP2 protein and nucleic acids of the invention are useful in the production of a transgenic animal which expresses ACP2 protein. The ACP2 nucleic acids of the invention are useful in the production of allele-specific oligonuclectides designed to genotype each of the ACP2 polymorphisms. Nucleic acids ABL36299-ABL36320 represent claimed ACP2 allele-specific probes. Nucleic acids ABL36321-acids ABL36364 represent claimed ACP2 allele-specific PCR primers. Nucleic acids ABL36329-ABL36321-acids ABL36364 represent claimed ACP2 allele-specific PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an isolated polynucleotide comprising a sequence
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for therapeutic purposes and for expressing SMOH protein useful in
identifying drugs to treat basal cell carcinomas.
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                                                                                                                                                                                                                                                                  32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMOH polymorphism detecting primer SEQ ID No 119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bentivegna SC, Choi JY, Koshy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL39804 standard; DNA; 10 BP.
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The invention relates to detecting CC (colorectal cancer e.g. colorectal adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC) or renal dipeptidase (RDP) in faeces or blood of a subject and comparing amount of MIC or RDP detected to that in normal subjects, where an elevated amount of MIC or RDP in the subject is an indicator of CC in subject; (b) isolating mRNA sample from faeces of a subject, detecting MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP mRNA in the subject is an indicator of CC in subject; (c) isolating epithelial cells from blood of a subject, isolating an mRNA sample from faeces of a subject or epithelial cells, detecting MIC or RDP mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in the mRNA sample.

The mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where an elevated amount of MIC or RDP mRNA in the mRNA sample or amounts of MIC or RDP mRNA in the mRNA sample or amount of MIC or RDP mRNA in the mRNA sample to amount of MIC or RDP mRNA in the blood or faeces of a subject; with an elevated amount of MIC or RDP mRNA in the blood or faeces of a subject sample comparing the amount of activity of RDP in the blood or faeces of the subject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting colorectal cancer in a subject, involves detecting macrophage inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood of the subject.
                 for determining whether an individual has one of the haplotypes or the haplotype pairs. The polymuclectides of the invention can be used to treat disorders by gene therapy and antisense gene therapy. This polymuclectide sequence represents a primer used for detecting human smoothened Drosophila homologue gene polymorphisms of the invention
  new method, an oligonucleotide and kit of the invention are useful
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                                                                                                                                                                               Score 8.4; DB 1; Length 10;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            ACA94693 standard; DNA; 10 BP.
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to that in normal subjects, where an elevated amount of activity of RDP subject; (e) administering to a subject is an indicator of CC in the subject; (e) administering to a subject an antibody which specifically binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is labeled with a moiety which is detectable from outside of the subject and acteding the moiety with in the subject from outside of the subject and area of localisation of the moiety within the subject but outside the proximal tubules of the kidney identifies CC; or (f) administering to a subject a substrate for RDP, the substrate being labeled with a detectable moiety, isolating faces or blood from the subject, and detecting in the faces or blood MDP reaction product or RDP substrate with the detectable moiety, where increased product or decreased cut the faces or blood indicates CC in the subject. The methods are useful for detecting colorectal cancer in a subject. The present sequence is a DNA tag derived from a human transcript whose expression is ö The invention relates to gonadotropin-releasing hormone 2 (GNRH2) and its nucleic acid sequence. Polymorphic variants of the GNRH2 gene are useful in studying the expression and function of GNRH2, and in expressing GNRH2 proteins for use in screening candidate drugs for treating diseases associated with GNRH2 activity, such as reproductive disorders. Polymucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a patient could benefit from expression or increased expression of a particular GNRH2 protein isoform, or an expression vector encoding the isoform may be administered to the New gonadotropin-releasing hormone 2 (GNRH2) polypeptide encoded by genetic variants having polymorphisms in the GNRH2 gene, for studying the function of, and treating disorders, such as, reproductive disorders. Human; gonadotropin-releasing hormone 2; GNRH2; reproductive disorder; gynaecological; cytostatic; hormonal; target validation; gene therapy; drug screening; lead compound; primer; ss. Gaps ;; 0 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels repressed in colorectal cancer or colorectal adenoma Human GNRH2 gene polymorphism detecting primer #13. Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other; Sausker EA; Nandabalan K, Claim 16; Col 14; 33pp; English. AAD53537 standard; DNA; 10 BP. (GENA-) GENAISSANCE PHARM INC 01-NOV-2001; 2001WO-US050630 18-MAY-2001; 2001WO-US016353. (first entry) Local Similarity 90.0 12 CCCCTTCCTA 21 10 CCCCATCCTA 1 WPI; 2003-148454/14. Duda A, Kliem SE, WO200294850-A2. 28-MAY-2003 28-NOV-2002 AAD53537; Query Match RESULT 403 Matches Homo AAD53537 셤 88888888888888888888888888

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patient. Haplotype information is useful in improving the efficiency and output of several steps in a drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. GNRH2 gene is used in gene therapy. The present sequence is a primer used for detecting human GNRH2 gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises a method for the PCR amplification of nucleic acids. The method involves a set of primers, where two of the primers are in solution and at least two other primers are atrached to a solid support. The method of the invention can be used for the analysis of a nucleic acid or a mixture of nucleic acids, including: single-stranded present DNA molecules, double-stranded DNA molecules, acut of the invention amplified polymorphic DNA (RAPD) PCR primer of the invention
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RNA analysis, RAPD, PCR, primer, random amplified polymorphic DNA.
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                                                                                                                                                                                                                                                                                                                           Hereditary factor marker for allergic diseases comprises polymorphism-containing DNA fragments of interleukin-4, IL-13, IL-4 receptor-alpha or-beta gene, or human signal transducer and activator of transcription 6
                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to hereditary factor markers (1) for allergic diseases comprising polymorphism-containing DNA fragments of Interleukin-4 (IL-4) (ADD32108 and ADD32129), IL-13 (ADD32113, ADD32114, ADD32128, ADD32129, ADD32124, ADD32124, IL-4 receptor alpha (ADD32128, ADD32129, ADD32133, ADD32134, ADD32138 and ADD32139), IL-3 receptor beta (ADD3213 and ADD32134) and ADD32134 and ADD32134 and ADD32149 are useful as a marker of hereditary factor of allergic diseases, thus are useful for detecting allergic diseases such as atopic dermatitis.
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                                                                                               Polymorphism; Interleukin-4; IL-4; Interleukin-13; IL-13; Interleukin-4 receptor alpha; IL-4 receptor alpha; Interleukin-3 receptor beta; IL-4 receptor beta; human; Signal Transducer and Activator of Transcription 6; STAT6; allergy; allergic disease; atopic dermatitis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
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                                                                           Polymorphic STAT6 gene fragment, SEQ ID 42.
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          ADD32149 standard; DNA; 10 BP.
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This invention relates to a novel method for the optimisation of primer libraries. Specifically, it refers to increasing the affinity of short oligonucleotide primers, also known as extendable oligos (BOS), for their template sequences. The present invention describes improved methods for sequenching and the linear and exponential amplification of DNA that can be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle amplification, strand displacement amplification and isothermal DNA amplification. Accordingly, these extendable oligos with improved specificity and affinity are particularly important in fields ranging from biotechnology and agriculture to medical research. This oligonucleotide sequence is an extendable oligonucleotide that includes an adenine replacement 2,4 diaminopurine nucleotide analogue in the catch region, and is useful for both DNA sequencing reactions and PCR amplification in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing the affinity of an extendable oligonucleotide (EO) for a target nucleic acid, for providing primers having improved specificity, comprises hybridization of the EO to a template oligonucleotide (TO) and extension of the EO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 9; Page 40; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN89103 standard; DNA; 10 BP.
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                                                                                                                                                     24-DEC-2002; 2002WO-AU001763
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                          (NUCL-) NUCLEICS PTY
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WO2003093500-A1
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Cappola G; : C, Petersen N; Messer C, Dain BJ, Lee HH, Litvyn L, N 30 DP, Windemuth AK; Bieglecki KM, Brain CD, Russo DP, Lachowicz M, Reed CR, Rounds EM, Bentivegna SC, Judson RS,

WPI; 2004-340942/31.

New Kit comprising a set of oligonucleotides, useful for determining whether an individual has a statin response marker I or II for preparing composition for treating hyperlipidemia.

Disclosure; SEQ ID NO 171; 202pp; English.

A kit comprising a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic sites (PS) in a set of lag bate one of the alleles at each polymorphic sites (PS) in a set of lag purpose of the alleles at each polymorphic sites (PS) in a set of polymorphic sites (PS) given in the specification, for each polymorphic sites comprising a linked haplotype for any one of haplotypes (DI) and PSA; PSI3 and PSA2; and PSA2; as set of polymorphic sites comprising a linked haplotype for any one of haplotypes (DI) 134, 201-463 or 501-515 given in the specification; or a set of polymorphic sites comprising a substitute haplotype for any one of haplotypes 101-134, 201-463 or haplotypes 501-515 given in the specification; where the nucleotide position of each polymorphic site comprising a substitute haplotype for any one of paplotypes 101-134, 201-463 or haplotypes 501-515 given in the specification; where the nucleotide position in the 3257-bp corresponds to the following nucleotide position in the 3257-bp corresponds to the following nucleotide position in the 3257-bp corresponds to the following nucleotide position in the 3257-bp corresponds to the following nucleotide position in the 3257-bp corresponds are at an included for: determining whether an individual has a stain response marker I or a stain response marker I or a stain response marker I or a stain response are at a stain response marker I or a stain response to treatment with a stain; manufacturing a drug product comprising a stain response marker I, an area of the following an individual? High Density Lipoprotein Cholesterol (HDLC) response to treatment with a stain; marketing a grain response marker I, an isolated polymuclocide comprising a stain response marker I, an isolated polymuclocide comprising a stain response marker I, an isolated polymuclocide comprising a stain response marker I, an isolated polymuclocide comprising a stain response marker I, an isolated polymuclocide seeking response marker I; an isolated polymuclo recombinant nonhuman organism transformed or transfected with the isolated polynuclectide, where the organism expresses an ITGB3 isolated polynuclectide, where the organism expresses an ITGB3 polypeptide encoded by the selected ITGB3 isogene; an isolated fragment comprises one or mom polymorphisms consisting of thymine at PS 1, quanine at PS 2, thymine at PS 3, thymine at PS 4, cytosine at PS 5, adenine at PS 6, thymine at PS 9, thymine at PS 9, adenine at PS 10, adenine at PS 11, thymine at PS 19, quanine at PS 10, adenine at PS 11, thymine at PS 19, quanine at PS 11, quanine at PS 19, quanine at PS 17, thymine at PS 19, adenine at PS 19, adenine at PS 19, thymine at PS 19, adenine at PS 10, adenine at P of isogenes 1-98, where each of the selected isogenes is defined by a correspondingly numbered haplotype given in the specification, and where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-13723, 1435-14858, 16126-16619, 1639-17414, 19241-19644, 19748-20177, 2053%21009, 21731-22412, 24385-24930, 2555926609, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence except where substituted

where the comparison of the correspondingly numbered hablotyee at each of file of an individual; assigning a haplotyee pair for the integril, beta of each of an individual; assigning a haplotyee pair for the integril, beta of the comparison and the comparison and the control of the control population partly or wholly defined by having a statin response marker I, where a trial population having the statin response marker substitution having the statin response marker exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. Preferred Oligonucleotide: The isolated oligonucleotide is an allele-specific alignment of a partle of the precipitation of the polymorphic site. The isolated oligonucleotide is a primer-extension oligonucleotide. The kit is for

CC comprises a set of oligonucleotides designed for identifying at least one comprises a set of oligonucleotides designed for identifying at least one comprises a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (BS) in a set of two or more has a statin response marker II comprises determining the copy number in the individual of the haplotype, where if the selected haplotype is one of haplotypes given in the specification, the selected haplotype is one of the selected haplotype and a statin response marker I if the individual has a statin response marker I if the individual has a statin response marker I if the individual has a statin response marker I if the individual has a statin response marker I if the individual has a statin response marker I if the individual has a statin response marker I if the individual has a statin response marker I if the individual is a candidate for treatment with a statin. The determining step comprises concerned to copy of the selected haplotype and using the results of the genotyping step to identify. For the set of polymorphic sites the haplotype and the individual. The determining step comprises consulting a data repository, that provides information on the copy number present in the individual or the selected haplotype. The data repository is the individual to a first or second statin response marker group if the individual has at least one copy of the selected haplotype and to the first statin response marker group if the individual has at least one copy of the selected haplotype and assigning the individual to the first statin response marker group if the selected haplotype and to the second statin response marker group if the selected haplotype and to the second statin response marker group if the selected haplotype and to the second statin response marker group if the selected haplotype and to the second statin response marker group if the selected haplotype and to the second statin response marker group if the selec ö Score 8.4; DB 1; Length 10; Pred. No. 2.5e+02; 0; Mismatches 1; Indels 32.3%; Query Match
Best Local Similarity 90.00,

Gaps

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ADS76817; RESULT 408

Breast cancer detection oligonucleotide #599.

ss; primer; cytostatic; RNA interference; RNA; gene silenci antisense oligomucleotide inhibitor; cathepsin K inhibitor; cathepsin L inhibitor; cathepsin F inhibitor; metalloprotease 2 inhibitor; thombospondin-2 antagonist; collagen antagonist; diagnosis; breast tissue; cancer.

Ното варіеля

20-MAR-2003; 2003US-0456735P.

Allinen M; Polyak K, Porter D,

WPI; 2004-728732/71

10 1 cccccrcarc 10 н ઠે g

ADS76817 standard; DNA; 10 BP (first entry) 30-DEC-2004

22-MAR-2004; 2004WO-US008866 WO2004085621-A2. 07-OCT-2004.

(DAND) DANA FARBER CANCER INST INC.

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Diagnosing breast cancer comprises determining expression levels of a gene selected from those differentially expressed in normal or cancerous cells of a breast tissue sample including interleukin 1, thrombospondin 1
                                                                                                                                                                 cystatin C.
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Example 2; SEQ ID NO 599; 149pp; English.

The invention relates to a method of diagnosis (M1) comprising: (a) providing a test sample of breast tissue; (b) determining the level of expression in the test sample of a gene (e.g. interleukins, superoxide dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the specification, and (c) if the gene is expressed in the test sample at a lower level than in a control normal breast tissue sample, diagnosing the test sample as containing cancer cells. The method is used for diagnosing breast cancer. This sequence corresponds to an oligonucleotide primer used in the method of the invention.

Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Gaps ö 32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.00,
Best Acan 9; Conservative

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ADS77906 standard; DNA; 10 BP. (first entry) 30-DEC-2004 ADS77906; RESULT 409

Breast cancer detection oligonucleotide #1688.

ss; primer; cytostatic; RNA interference; RNAi; gene silencing; antisense oligonucleotide inhibitor; cathepsin K inhibitor; cathepsin F inhibitor; metalloprotease 1 inhibitor; thrombospondin-2 antagonist; collagen antagonist; diagnosis; breast tissue; cancer.

Homo sapiens.

WO2004085621-A2.

07-OCT-2004.

22-MAR-2004; 2004WO-US008866

(DAND) DANA FARBER CANCER INST INC.

20-MAR-2003; 2003US-0456735P.

CCCCCCXXX4444X8X6X8X6X6X6X8X8X8X8X8X8X8X8XCCCCCC

Ξ Porter D, Allinen Polyak K,

WPI; 2004-728732/71.

Diagnosing breast cancer comprises determining expression levels of a gene selected from those differentially expressed in normal or cancerous cells of a breast tissue sample including interleukin 1, thrombospondin 1 Diagnosing breast cancer gene selected from those and cystatin

Example 6; SEQ ID NO 1688; 149pp; English.

The invention relates to a method of diagnosis (M1) comprising: (a) providing a test sample of breast tissue; (b) determining the level of expression in the test sample of a gene (e.g. interleukin-8, superoxide dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the specification, and (c) if the gene is expressed in the test sample at a lower level than in a control normal breast tissue sample, diagnosing the

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screening;
                                                                                 ADU19887;
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                                  RESULT 41
ADU19887/
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breast cancer. This sequence corresponds to an oligonuclectide primer used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing breast cancer comprises determining expression levels of a gene selected from those differentially expressed in normal or cancerous cells of a breast tissue sample including interleukin 1, thrombospondin 1
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                         88; primer; cytostatic; RNA interference; RNAi; gene silencing; antisense oligonucleotide inhibitor; cathepsin K inhibitor; cathepsin L inhibitor; cathepsin F inhibitor; metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
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                                                                               Query Match 32.3%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                         collagen antagonist; diagnosis; breast tissue; cancer.
                                                        Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                    Breast cancer detection oligonucleotide #1025
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                                                                                                                                                                                                             ADS77243 standard; DNA; 10 BP.
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Matches 9; Conserv
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The invention comprises a method of screening for candidate agents capable of altering the biological activity of a protein encoded by a nucleotide involved in hypoxia-related tumourigenesis. The method of the involves is contacting a test agent with a target cell expressing the nucleotide, and monitoring the activity of the expressed protein product; if the test agent modifies the activity of the expressed protein then this is a candidate agent. The method of the invention is useful for modifying hypoxia-induced gene regulation and for diagnosing, prognosing or treating tumours. The present DNA sequence represents a SAGE tag that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying agents that alter biological activity of a polypeptide encoded by a polynucleotide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                       Hypoxia-related tumourigenesis-related SAGE tag #1678
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hypoxia-induced gene regulation; tumour; SAGE tag; ds.
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90.0%;
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ADU19887 standard; DNA; 10
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Best Local Similarity
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                                                                                                                        13-JAN-2005
                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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The invention comprises a method of screening for candidate agents capable of altering the biological activity of a protein encoded by a nucleotide involved in hypoxia-related tumourigenesis. The method of the invention involves: contacting a test agent with a target cell expressing the nucleotide, and monitoring the activity of the expressed protein product; if the test agent modifies the activity of the expressed protein product; is a candidate agent. The method of the invention is useful for modifying hypoxia-induced gene regulation and for diagnosing, prognosing or treating tumours. The present DNA sequence represents a SAGE tag that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining whether an individual has a response marker I or II comprises determining whether the individual has zero copies or at least one copy
                          Identifying agents that alter biological activity of a polypeptide encoded by a polynucleotide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholinergic receptor, nicotinic, alpha polypeptide 2; CHRNA2; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CHRNA2 gene PS6 detecting reverse primer extension, SEQ ID NO: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selectable marker; pharmaceutical; gene therapy; diagnosis; SNP detection; cognitive discorder; nootropic; neurological di dementia; Alzheimers disease; neuroprotective; degeneration; parkinsons disease; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                    32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
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Reed CR;
                                                                                                                   Disclosure; Page 70; 100pp; English
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Ozdemir V,
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                                                                                     expressed product.
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ATHANASIOU M.
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DENTON R R.
JUDSON R S.
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COHEN N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises a method of screening for candidate agents capable of altering the biological activity of a protein encoded by a nucleotide involved in hypoxia-related tumourigenesis. The method of the invention involves: contacting a test agent with a target cell expressing the nucleotide, and monitoring the activity of the expressed protein product; if the test agent modifies the activity of the expressed protein then this is a candidate agent. The method of the invention is useful for modifying hypoxia-induced gene regulation and for diagnosing, prognosing or treating tumours. The present DNA sequence represents a SAGE tag that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                             Identifying agents that alter biological activity of a polypeptide encoded by a polynucleotide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity of expressed product.
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hypoxia-induced gene regulation; tumour; SAGE tag; ds
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Best Local Similarity 90.0
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Unidentified
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sub-family A (ABC1),
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                                           The present invention relates to a method for determining whether an individual has a response marker I or II. The method involves determining whether the individual has zero copies or at least one copy of any of the choinergic receptor, nicotinic, alpha polypeptide 2 (CHRMA2) haplotypes. The composition and methods are useful for diagnosing and treating a cognitive disorder, e.g. mild or moderate dementia of the Alzheimer's type, or dementia associated with Parkinson's disease. The method of the invention is also useful for predicting the expected therapeutic response of an individual to treatment with galantamine and for gene therapy. The present sequence is the human CHRNA2 gene polymorphic site 6 (PS6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of analyzing haplotype, by detecting gene polymorphism in drug-related genes such as aryl acetylamide deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analyzing haplotype, by detecting polymorphism in drug-related genes, electing common polymorphism (CP), building haplotype block using CP, specifying CP within block, specifying tag polymorphism from CP within
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm; immune disorder; cardiovascular disease; metabolic disorder; respiratory disease; musculoskeletal disease; renal disease; nephrotropic; endocrine disease; genitourinary disease.
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                                                                                                                                                                                                             32.3%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               Human SNP detection related oligonucelotide #1386.
                                                                                                                                                                                      Sequence 10 BP; 0 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 1386; 1290pp; Japanese.
                                                                                                                                                               detecting primer extension oligonucleotide.
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                       SEQ ID NO 26; 52pp; English.
of any of the CHRNA2 haplotypes.
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28-MAY-2004; 2004JP-00158717.
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STAGEN CO LTD.
SEKINE A.
IIDA A.
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Matches 9; Conserv
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                        Claim 42;
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ö haplotype. The method is useful for estimating the sensitivity or disease of a medicine or a foreign material, for selecting medicine for preventing or treating disease, for determining appropriate dosage of medicine for preventing or treating a disease, for analyzing a drug interaction, and for determining the related polymorphism relative to the sensitivity of the medicine, foreign material or disease. The diseases include malignant tumor, immune disorder circulatory disease, metabolic disease, kidney disease, respiratory disease and muscle associated disease. The method enables analysis of the individual differences related to the sensitivity of a medicine, using a haplotype, without using each single nucleotide polymorphism. The present sequence represents a human SNP detection related oligonucelotide. Triplex formation; DNA detection; triple helix; identification; bacteria; The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex stability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The sasay comprises adding a sample containing double-stranded DNA test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of Gaps Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify member 1. The method is useful for analyzing . 0 Triple helix third strand of HER-2 gene nucleotides 4250-4260. Score 8.4; DB 1; Length 10; Pred. No. 2.5e+02; 0; Mismatches 1; Indels Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other; Disclosure; Col 15-16; 168pp; English INC. (PROF-) PROFILE DIAGNOSTIC SCI BP. 32.3%; 93US-00173489. 92US-00968436. AAX14673 standard; DNA; 11 (first entry) Local Similarity 90.0 3 ACCTCATCGC 12 Н 88. Hepburn AG, Wang C; 10 ACCACATCGC WPI; 1999-130384/11. oncogene; virus; Homo sapiens 22-DEC-1993; 24-MAR-1999 29-OCT-1992; US5861244-A. 19-JAN-1999. Synthetic AAX14673; bacteria. Query Match

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This invention describes a novel method allowing essential or functional genes to be rapidly identified and inactivated. The method is able to firstly identify most of the essential genes in an organism (i.e. a bacteria or a eukaryote) needed for survival, and secondly it provides for reducing or inactivating their expression. The method is able to identify functional olisonucleotide molecules able to be used as diagnostic reagents and therapeutics. The method provides a means for identifying essential genes whose sequence is known only as part of a genome with unknown function, as well as a means for identifying uncleic acid molecule comprising (a) a first reporter gene encoding a functional oligonucleotide molecules. The method involves the use of a nucleic acid molecule comprising (a) a first reporter gene encoding a fusion protein comprising a protein of interest (itself translated from a RNA of interest) and a reporter protein, as second reporter gene encoding a functional oligonucleotide molecule such as an external guide sequence functional oligonucleotide molecule such as an external guide sequence functional oligonucleotide molecule such as an external guide sequence.
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the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of
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Pred. No. 2.5e+02;
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                                                           oncogenes and Hepatitis B virus
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                                                                                                                                    32.3%;
90.0%;
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9; Conserve
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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or commettic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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                                                                                                                                                                                                                        Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                                                                                                                         Human skin stress/ageing related EST SEQ ID NO 255.
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0; Mismatches
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                                                                                                  ABQ86500 standard; cDNA; 11 BP.
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nes 9; Conservative
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1 CCACCTCATC
                  CCACGTCATC
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Best Local Similarity Matches 9; Conserv

Query Match

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20-DEC-2001; 2001WO-EP015178.
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Best Local Similarity
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                                            screening for expression.
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                                                                                                                                                                                                                                                                 Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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   88.
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Human; skin ageing; skin stress; EST; expressed sequence tag;
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                                                                                                                                                                                                          Hofmann K;
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                                                                                                                                                                                                                                                                                                                             Claim 8; Page 39; 325pp; German.
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Best Local Similarity 90...
Best Local 9; Conservative
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                             Homo sapiens
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Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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                                                                                                                                                                                           Claim 8; Page 89; 325pp; German.
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ABV67130 standard; cDNA; 11 BP.
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Best Local Similarity
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                                                                            ABV67130;
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pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintenis or promotes skin homeostasis or that can be used for treating skin electrically neurodermatitis; sumburn; psoriasis; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ichthyosis, atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                              Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                        Query Match 32.3%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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                                                  Sequence 11 BP; 2 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                              Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; seleroderma;
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immunosuppressive; antiinflammatory; cytostatic; SAGB; neurodermatitis;
psoriasis; dermatitis; skin cancer; BST; expressed sequence tag; ss.
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Sequence 11 BP; 3 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

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32.3%;
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 Query Match 32.3
Best Local Similarity 90.0
Matches 9; Conservative
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Pred. No. 2.5e+02;
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WO200253774-A2
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promote skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to tast agent (A) that maintains or promotes skin homeostasis and to tast subburn; psoriasis, selexoderma; ichthyosis; atopic dermatitis; aunburn; psoriasis; scleroderma; lichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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ö Gaps ; 0 Score 8.4; DB 1; Length 11; Pred. No. 2.5e+02; 0; Mismatches 1; Indels .. 32.3%; 90.0%; 9; Conservative 21 CCCCATCCTA 1 CCCCTTCCTA Query Match Best Local Similarity 10

BP. ABV68137 standard; cDNA; 11 (first entry) Human skin EST 5923. 21-OCT-2002 ABV68137;

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss.

Homo sapiens

WO200253774-A2

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127

(HENK) HENKEL KGAA.

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WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 189; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or

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                 disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; sosceat, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                           Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Pred. No. 2.5e+02;
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90.0%;
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                                                                                                                                                                                                                                                                                                                                    Petersohn D, Conradt
                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-590638/63.
                                                                                                                                                                                                                                                                                                              (HENK ) HENKEL KGAA
                                                                                                                                        Human skin EST 7613
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    e.g. skin cancer.
                                                                                                                                                                                                                          WO200253774-A2.
                                                                                                                                                                                                      Homo sapiens.
                                                                                                                  21-OCT-2002
                                                                                                                                                                                                                                               11-JUL-2002
16
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                                                                                             ABV69827;
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; icosacea, metanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 BP; 0 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 209; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hofmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV71899 standard; cDNA; 11 BP
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2001; 2001WO-EP015179.
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Sequence 11 BP; 2 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           Human Pan-Endothelial Marker SEQ ID NO 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinzler KW, Vogelstein B;
                                 Hofmann K;
                                                                                      Claim 24; Page 313; 1345pp; German.
                                                                                                                                                                                                                                                                                   ABL91969 standard; cDNA; 11 BP.
       03-JAN-2001; 2001DE-01000127.
                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-2001; 2001WO-US024031.
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11-APR-2001; 2001US-0282850P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                             30-MAY-2002 (first entry)
                                 Conradt M,
                                                                                                                                                                                                                        Conservative
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                    (HENK ) HENKEL KGAA.
                                               WPI; 2002-590638/63.
                                                                                                                                                                                                                                     11 GCCCCTTCCT
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                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                          e.g. skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                               WO200210217-A2.
                                 Petersohn D,
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90740, ABB907450 and ABB907650. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, necangiogenesis in subjects bearing a vascularised tumour, polycystic Kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonuclectide sequences: tumour endothelial markers (TEM) ABL92045-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL91995-ABL92044; and pan-endothelial markers (PEM) ABL91995. The present sequence is that of an
An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; necangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.3%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA tag used to identify human gene encoding PEM 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 BP; 2 A; 1 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligonucleotide marker useful to the invention
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                                                                                                   Example 4; Page 326; 331pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-2002; 2002WO-US008253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 90.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CATCCTAAGC
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                                                                                                                                                                                                                                                                                                                                           The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaris; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
normal endothelial marker; pan-endothelial marker; immunostimulant;
antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                        In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or

Disclosure; Page 97; 374pp; English

psoriasis

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Gaps

ö This invention describes a novel in vitro method for identifying genes that are significant for hair-bearing skin in humans. The method comprises recovering, from hair-bearing skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from skin on which hair does not grow and subjecting both mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between the two types of skin. The invention also describes in vitro methods for determining homeostasis of human hair-bearing skin and for determining activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human hair-bearing skin. A biochip and a test kit comprising a solid support (flexible or rigid) with In vitro identification of genee important for hair-bearing skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis. The present invention relates to a novel method for the isolation of endothelial cells (BCB), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (DEM), normal endothelial marker (DEM), normal consistency of the properties of the properties are identified in human ECs. The human EC marker proteins and the jobynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting necangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. ABX71828-ABX71999 represent DNA tags for human PEM, TEM or NEM genes Gaps hair-bearing skin; human; serial analysis of gene expression; SAGE; homeostasis; cosmetic; pharmaceutical; biochip; ds. ; Human hair-bearing skin-associated DNA fragment SEQ ID NO 50. Holtkoetter 0; 32.3%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels Sequence 11 BP; 2 A; 1 C; 5 G; 3 T; 0 U; 0 Other; Gassenmeier T, Claim 8; SEQ ID NO 50; 250pp; German. ADQ35233 standard; DNA; 11 BP. 20-DEC-2002; 2002DE-01060931. 20-DEC-2002; 2002DE-01060931 Schlotmann K, (first entry) Query Match
Best Local Similarity 90.0
Matches 9; Conservative 24 Hofmann K; ~ (HENK) HENKEL KGAA. WPI; 2004-518857/50. 11 CATCCTAAGC 15 CTTCCTAAGC DE10260931-A1 Homo sapiens. Petersohn D, 23-SEP-2004 08-JUL-2004 Conradt M, ADQ35233; RESULT 439 ઠે 셤 88888888888888888888

This invention describes a novel in vitro method for identifying genes
that are significant for hair-bearing skin in humans. The method
comprises recovering from hair-bearing skin in humans. The method
comprises recovering from hair-bearing skin a first mixture of
genetically expressed (transcribed and optionally translated) factors
(i.e. proteins, mRNA or their fragments), recovering a second, similar
mixtures from skin on which hair does not grow and subjecting both
mixtures to serial analysis of gene expression (SAGE) to identify those
competed from skin on which hair does not grow and subjecting both
mixtures to serial analysis of gene expression (SAGE) to identify those
conserts which expression is markedly different between the two types of
the invention also describes in vitro methods for determining
commetic and pharmaceutical agents for use against disorders or
commetic and pharmaceutical agents for use against disorders or
disturbances of the homeostasis of human hair-bearing skin, a biochip and
a test kit comprising a solid support (flexible or rigid) with
confined probes are also described for determining homeostasis. The
immobilised probes are also described for determining homeostasis. The
confined allows identification of as many as possible of the genes
confined therapeutic and cosmetic agents. ADQ355184-ADQ36518 represent ö In vitro identification of genes important for hair-bearing skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis. immobilised probes are also described for determining homeostasis. The hair-bearing skin is from the scalp and the other skin is from the face. The method allows identification of as many as possible of the genes important for hair-bearing skin, and therefore, of a very wide range of potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent human DNA, Tag fragments used to identify genes associated with hair-Gaps hair-bearing skin; human; serial analysis of gene expression; SAGE; homeostasis; cosmetic; pharmaceutical; biochip; ds. ö Human hair-bearing skin-associated DNA fragment SEQ ID NO 330. Gassenmeier T, Holtkoetter O; Score 8.4; DB 1; Length 11; Pred. No. 2.5e+02; 1; Indels Sequence 11 BP; 0 A; 5 C; 3 G; 3 T; 0 U; 0 Other; 0; Mismatches Claim 5; SEQ ID NO 330; 250pp; German. BP. 20-DEC-2002; 2002DE-01060931. 32.3%; 90.0%; 20-DEC-2002; 2002DE-01060931 Schlotmann K, ADQ35513 standard; DNA; 11 23-SEP-2004 (first entry) 9; Conservative 1 D, Schar M. Hofmann K; 20 GCCCTTCCT 11 (HENK) HENKEL KGAA. 11 GCCCCTTCCT WPI; 2004-518857/50. Query Match Best Local Similarity DE10260931-A1 bearing skin Homo sapiens 08-JUL-2004. Petersohn D Conradt M, ADQ35513; Matches ADQ35513/ 888888888888 ਠੋ 셤

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   In vitro identification of genes important for hair-bearing skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
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                                                                                                                                         Gaps
 human DNA Tag fragments used to identify genes associated with hair-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hair-bearing skin; human; serial analysis of gene expression; SAGE; homeostasis; cosmetic; pharmaceutical; biochip; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human hair-bearing skin-associated DNA fragment SEQ ID NO 400.
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                                                                                           32.3%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                       Sequence 11 BP; 3 A; 0 C; 8 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                          ADQ35583 standard; DNA; 11 BP.
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                                                                                                                                     9; Conservative
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                                                                                                         Best Local Similarity
Matches 9: Conser
                   bearing skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petersohn D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                               Query Match
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SXXX
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Sequence 11 BP; 3 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

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This invention describes a novel in vitro method for identifying genes
that are significant for facial skin in humans. The method comprises
crecovering, from facial skin, a first mixture of genetically expressed
(transcribed and optionally translated) factors (i.e. proteins, mRNA or
their fragments), recovering a second, similar mixture from some other
brans and subjecting the mixtures to serial analysis of gene expression
(SAGE) to identify those genes for which expression is markedly different
between facial skin and the other tissue. The invention also describes an
in vitro method for determining homeostasis of human facial skin; a test
kit which comprises a solid support (flexible or rigid) on which are
immobilised probes that bind specifically to the factors of interest and
biochip for determining homeostasis of human facial skin; a test
committed probes that bind specifically to the factors of interest and
cof the invention are also used in a method which determines activity of
cosmetic and pharmaceutical agents for use against disorders or
cof asturbances of the homeostasis of human skin and a screening method for
identifying cosmetic and pharmaceutical agents. The method allows
clantifying cosmetic and pharmaceutical agents. The method allows
shin and thus of a very wide range of potential therapeutic and cosmetic
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                                           Gaps
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32.3%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.5e+02; 1: Indels
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                                                                                                                                                                                                                                                                                                                                             Human facial skin-associated DNA fragment SEQ ID NO 2040.
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                                                                                                                                                                                                                       ADQ33950 standard; DNA; 11 BP
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Matches 9; Conservative
                                                                             17 TCCTAAGCAT 26
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Conradt M, Hofmann K;
                                                                                                        TACTAAGCAT
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(first entry)

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In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
                                                                                                                                                                                                                                          facial skin; human; serial analysis of gene expression; SAGE; homeostasis; biochip; cosmetic; pharmaceutical; ds.
                                                                                                                                                                                                Human facial skin-associated DNA fragment SEQ ID NO 1986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; SEQ ID NO 1986; 577pp; German.
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                                                                ADQ33896 standard; DNA; 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel in vitro method for identifying genes recovering, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin, a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of
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                                                                                                                                                       ADQ33674 standard; DNA; 11 BP.
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4 CCTCATCGCC 13
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Best Local S:
Matches 9
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Gassenmeier T, Holtkoetter O;

Schlotmann K,

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This invention describes a novel in vitro method for identifying genes recovering, from facial skin, in humans. The method comprises recovering, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin, a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic agents. AD031911-AD035111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention.
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ID ADQ33355 standard; DNA; 11 BP.
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ADQ33355;

08-JUL-2004

Conradt M,

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This invention describes a novel in vitro method for identifying genes
that are significant for facial skin in humans. The method comprises
cc that are significant for facial skin in humans. The method comprises
cc trecovering, from facial skin, a first mixture of genetically expressed
(transcribed and optionally translated) factors (i.e. proteins, mRNA or
their fragments), recovering a second, similar mixture from some other
thuman tissue, preferably skin from a protected area, especially from the
breast and subjecting the mixtures to serial analysis of gene expression
(SAGE) to identify those genes for which expression is markedly different
between facial skin and the other tissue. The invention also describes an
in vitro method for determining homeostasis of human facial skin; a test
kit which comprises a solid support (flexible or rigid) on which are
immobilised probes that bind specifically to the factors of interest and
a biochip for determining homeostasis of human facial skin. The products
of the invention are also used in a method which determines activity of
cosmetic and pharmaceutical agents for use against disorders or
identification of as many as possible of the genes important for facial
continued thus of a very wide range of potential therapeutic and cosmetic
continued thus of a very wide range of potential therapeutic and cosmetic
continued the facial standard and plantification is agents in the facial
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                                                                       facial skin; human; serial analysis of gene expression; SAGB;
homeostasis; biochip; cosmetic; pharmaceutical; ds.
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                       Human facial skin-associated DNA fragment SEQ ID NO 3051.
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                                                                                                                                                              Homo sapiens
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homeostasis; biochip; cosmetic; pharmaceutical; ds.
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                                                                                                                     Human facial skin-associated DNA fragment SEQ ID NO 1445.
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                                                                                                                                                                                                                                                                Homo sapiens
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Gaps ö

1; Indels

ADQ34961;

RESULT 446

ADQ34961,

Query Match

Best Loc Matches

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DE10260928-A1.

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This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises recovering, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, maNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin, a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human skin and a screening method for identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic gents. App31911-ApD35111 represent human DNA Tag fragments used to
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                                                                                                                                                                                                                                                                                                                                                      In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
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                                                                                                                                                                                                                                                               Schlotmann K, Gassenmeier T, Holtkoetter O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8.4; DB 1; Length 11;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human facial skin-associated DNA fragment SEQ ID NO 2445.
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homeostasis; biochip; cosmetic; pharmaceutical; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID NO 634; 577pp; German.
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                                                                                                                                                    20-DEC-2002; 2002DE-01060928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.3%;
90.0%;
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Best Local Similarity
                                                                          DE10260928-A1
                                      Homo sapiens.
                                                                                                                                                                                                                                                                 Petersohn D,
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Matches
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This invention describes a novel in vitro method for identifying genes
that are significant for facial skin in humans. The method comprises
crecovering, from facial skin, a first mixture of genetically expressed
(transcribed and optionally translated) factors (i.e. proteins, mRNA or
their fragments), recovering a second, similar mixture from some other
than tissue, preferably skin from a protected area, especially from the
breast and subjecting the mixtures to serial analysis of gene expression
(SAGE) to identify those genes for which expression is markedly different
control of the determining homeostasis of human facial skin; a test
in vitro method for determining homeostasis of human facial skin; a test
ckit which comprises a solid support (flexible or rigid) on which are
immobilised probes that bind specifically to the factors of interest and
a biochip for determining homeostasis of human facial skin; a test
commetic and pharmaceutical agents for use against disorders or
commetic and pharmaceutical agents for use against disorders or
identifying cosmetic and pharmaceutical agents. The method allows
clastifying cosmetic and pharmaceutical agents. The method allows
clastification of as many as possible of the genes important for facial
control of the interpret of the stange of potential therappeutic and cosmetic
                                                                                                                                                                                                                                                                                          In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention.
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                                                                                                                                                                                            Holtkoetter 0;
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                                                                                                                                                                                            Gassenmeier T,
                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 2445; 577pp; German.
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90.0%;
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Conradt M, Hofmann K;
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Best Local Similarity
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                                                                                                                                                                                                                                                       This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises that are significant for facial skin in humans. The method comprises contected area state of transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering is proteins in mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes and vitro method for determining homeostasis of human facial skin; a test kit which comprises a solid support (flexible or rigid) on which are continuouslised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use signist disorders or identifying cosmetic and pharmaceutical agents. The method allows identifying cosmetic and pharmaceutical agents for use sense in the formostasis of human skin and a screening method for identification of as any as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic dentify the facial skin-associated genes described in the invention.
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                                                                                                                                                                 In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
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                                                                                            Gassenmeier T, Holtkoetter O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.3%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human facial skin-associated DNA fragment SEQ ID NO 2564.
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                                                                                                                                                                                                                             Claim 5; SEQ ID NO 1984; 577pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ34474 standard; DNA; 11 BP
20-DEC-2002; 2002DE-01060928.
                             20-DEC-2002; 2002DE-01060928
                                                                                          Schlotmann K,
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Matches 9; Conservative
                                                                            Petersohn D, Schloum
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                                                             (HENK ) HENKEL KGAA.
                                                                                                                                       WPI; 2004-518855/50.
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This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises that are significant for facial skin in humans. The method comprises contracting, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA) or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGB) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes and via vitro method for determining homeostasis of human facial skin; a test immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or identifying cosmetic and pharmaceutical agents. The method allows cidentifying cosmetic and pharmaceutical agents for use against disorders of identification of as many as possible of the genes important for facial skin and thus of a very wide range of the genes important for facial skin and thus of a very wide range of petential therapeutic and cosmetic dentify the facial skin-associated genes described in the invention.
                                                                                                                                                                                                          In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                              Gassenmeier T, Holtkoetter O;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 BP; 3 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 2564; 577pp; German.
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                                                          Schlotmann K,
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                                                                                        Hofmann K;
(HENK ) HENKEL KGAA.
                                                                                                                                                      WPI; 2004-518855/50.
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                                                              Petersohn D,
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Matches
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                                                                                                                         The invention relates to a method of diagnosis (MI) comprising: (a) providing a test sample of breast tissue; (b) determining the level of expression in the test sample of a gene (e.g. interleukin.e, superoxide dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the specification, and (c) if the gene is expressed in the test sample at lower level than in a control normal breast tissue sample, diagnosing the test sample as containing cancer cells. The method is used for diagnosing breast cancer. This sequence corresponds to an oligonucleotide primer used in the method of the invention.
                                                 Diagnosing breast cancer comprises determining expression levels of a gene selected from those differentially expressed in normal or cancerous cells of a breast tissue sample including interleukin 1, thrombospondin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analyzing haplotype, by detecting polymorphism in drug-related genes, electing common polymorphism (CP), building haplotype block using CP, specifying CP within block, specifying tag polymorphism from CP within
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm; immure disorder; cardiovaecular disease; metabolic disorder; respiratory disease; musculloskeletal disease; renal disease; nephrotropic; endocrine disease; genitourinary disease.
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0
                                                                                                                                                                                                                                                      Score 8.4; DB 1; Length 11;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito S, Nakamura Y, Kamatani N;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SNP detection related oligonucelotide #1414.
                                                                                                                                                                                                                                   Sequence 11 BP; 1 A; 7 C; 1 G; 1 T; 0 U; 1 Other;
                                                                                                     Example 6; SEQ ID NO 1815; 149pp; English.
            Allinen M;
                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                        32.3%;
90.0%;
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28-MAY-2004; 2004JP-00158717
                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 90.00,
                                                                                                                                                                                                                                                                                                                                                                         ADZ24447 standard; DNA; 11
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SEKINE A.
            Porter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-305936/31.
                             WPI; 2004-728732/71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAITO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2005030952-A1
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                                                                                   and cystatin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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         Polyak K,
                                                                                                                                                                                                                                                                                                                                                                                               ADZ24447;
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(STAG-)
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(SAIT/)
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The invention relates to a method of analyzing haplotype, by detecting gene polymorphism in drug-related genes such as aryl acetylamide deacetylase, arylalkylamine N'acetyl transferase or Ary-binding cassette, sub-family 4 (ABCI), member 1. The method is useful for analyzing haplotype. The method is useful for estimating the sensitivity or disease of a medicine or a foreign material, for selecting medicine for preventing or treating diseases, for determining appropriate desage of medicine for preventing or treating a disease, for analyzing a drug interaction, and for determining the related polymorphism relative to the sensitivity of the medicine, foreign material or disease. The diseases include malignant tumor, immune disorder circulatory disease, metabolic disease. The method enables analysis of the individual differences related to the sensitivity of a medicine, using a haplotype, without using each single nucleotide polymorphism. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonuclectides of series 3, AAT63030-37, have specific anti-mRNA sequences to the 3' untranslated region (nucleotides 1489-1585) of tumour necrosis factor (TNF)-alpha mRNA. These oligonucleotides are an example of a new chimeric oligonucleotide library, used to identify an antisense binding site in a target mRNA (in this case TMF-alpha). The library comprises a set of distinct chimeric oligonucleotides capable of hybridising to mRNA to form a duplex, the nucleotide sequences of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor alpha; TNF-alpha; therapeutic agent; chimeric oligonucleotide library; antisense binding site; antisense compound; drug target validation; 3' untranslated region; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
Disclosure; SEQ ID NO 1414; 1290pp; Japanese.
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Query Match
                    RESULT 454
              Matches
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The invention provides a method for the differential screening of gene expression by random primed reverse transcription PCR (RT-PCR). The primer sequences are generated by stimulating PCR reactions on non-redundant mammalian nucleotide sequence databank entries containing at cleast 1,000 bp of coding region. The primers selected, such as the present one, had to meet various criteria such as having an efficiency index between 2-10, having a selectivity index higher than 1, being 12 bp long i.e. 8 C or G and 4 T or A, and each primer differed from the others in at least 5 of the 8 bases at the 3'-end. The invention claims the selected primers make it possible to use internally primed, PCR-based RNA fingerprinting for simple, exhaustive and systematic analysis of differential gene expression as an advantageous alternative to differential display. The method can also be useful for isolating new coding sequences and to compare known and new genes ö Differential screening of gene expression by reverse transcription polymerase chain reaction - uses random priming with primers selected for high efficiency and selectivity by computer screening of database(s). each have a common length of 7-20 bases. All of the nucleotides of the common length which are present as subsequences in the target mRNA are present in the library. Each nucleotide sequence comprises a recognition region recognisable by a duplex-cutting RNAse, and a flanking region of chemically modified nucleotides which binds to the mRNA sufficiently tightly to stabilise the duplex for the RNAse. Each oligonucleotide is protected against exonuclease attack. The libraries can be used to identify optimal effective antisense compounds against specific mRNA targets. The antisense compounds are useful as potential therapeutic agents, and as tools for drug target validation RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting; differential gene expression; ss. Gaps ö 32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; Live 0; Mismatches 1; Indels Random primed reverse transcription PCR primer 31. Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other; (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR. Claim 9; Page 24; 37pp; English. AAV32291 standard; DNA; 12 BP. 97WO-EP005290 96GB-00020216, (first entry) Local Similarity 90.0 14 CCTTCCTAAG 23 10 CTTTCCTAAG 1 Consalez G, Fesce R; WPI; 1998-230725/20. WO9813521-A1 26-SEP-1997; 27-SEP-1996; 18-AUG-1998 02-APR-1998 Synthetic. AAV32291;

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This sequence represents a chimeric antisense oligonucleotides, of the invention, that is an inhibitor of tumour necrosis factor alpha (TNF-alpha; Compositions, containing the chimeric antisense oligonucleotides and a duplex cutting enzyme, are useful in the treatment of disorders associated with expression of TNF-alpha (especially in keratinocytes). Such disorders are, e.g. inflammatory skin disorders, cachexia, an cautoimmune disorder, meningococcal septiceamia, a pulmonary inflammatory skin disorders, e.g. psoriasis, eczema and ultraviolet erythema. Once the mRNA is cut by the RNAse in the chimeric antisense oligonucleotide to bind another mRNA, Hence the chimeric antisense oligonucleotide acts catalytically. The antisense cligonucleotide acts catalytically. The antisense oligonucleotide acts catalytically. The antisense chimeric antisense oligonucleotide acts catalytically. The antisense chimeric antisense chimeric antisense chimeric antisense chimeric antisense chimeric antisense chimeric acts catalytically. The antisense chimeric antisense chimeric antisense chimeric antisense chimeric acts catalytically are antisense.
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                                                                                                                                                                                                                                                                                                                                                                TWF-alpha; inhibitor; chimeric antisense oligonucleotide; septic shock; tumour necrosis factor alpha; inflammatory skin disorder; cachexia; autoimmune disorder; meningococcal septicaemia; rheumatoid arthritis; pulmonary inflammatory disorder; graft versus host disease; lymphoma; psoriasis; eczema; ultraviolet erythema; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric antisense oligonucleotides against tumor necrosis factor alpha useful for treating inflammatory skin disorders.
                                           Gaps
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   Score 8.4; DB 1; Length 12;
Pred. No. 2.5e+02;
1; Mismatches 2; Indels
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                                       2; Indels
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98GB-00001617.
   32.3%;
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                                                                                                                                                                                                                                                                                                                                TNF-alpha inhibitor Z8903.
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                                         Conservative
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Matches 9; Conservative
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Query Match
Best Local Similarity
Matches 9; Conserv
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26-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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ID AAX7
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Sequence 12 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 1 Other;

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The invention relates to novel immunogenic CpG oligodeoxynucleotides

(AAC80581-C80723). The oligonucleotide are at least 10 bases long and

comprise one of the generic sequences 5.*NNNT-vpG-wNNN-3' or 5.*RY-CpG-RY

-3. The central CpG motif is unmethylated, and the oligonucleotides

coptionally have phosphorothioate linkages which make them more resistant

to degradation. The invention also relates to an oligonucleotide delivery

complex comprising an oligonucleotide of the invention and a targetting

agent, and a pharmaceutical composition comprising the oligonucleotide

delivery complex. The oligonucleotides are able to induce either a cell-

agent, and a pharmaceutical composition comprising the oligonucleotide

collimediated (T-cell) response or a humoral (B-cell, antipody) response, with

coligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a

cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNN-3'

being able to induce a humoral response. It is thought that after

administration, the oligonucleotide acts on antigen-presenting cells

cell-mediated nesponse and dendritic cells), which then release cytokines,

leading to activation of natural killer (RK) cells. A cell-mediated or

humoral response can then occur by activation of T- or B-cells. The

cinduction of an immune response is useful for treating, preventing or

ameliorating an allergic reaction (preferably asthma), or an infection,

where an immunospenic CpG oligonucleotide is administered either alone or

cin combination with an anti-allergenic agent or anti-infectious agent.

The allergic conditions which may be treated include eczema, allergic

rhinitis, hayfever, urticaria, food allergies and other atopic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic: cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; Humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple solerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiathmatic; dermatological; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:135.
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14 CCTTCCTAAG 23
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Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent. CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; B-cell response; antibody production; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiasthmatic; dermatological; phosphorothioate; ss. lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to bacterial, fungal and protozoal infections such as tuberculosis, AIDS, leishmania and schistosomiasis. Immune response induction may also be used in the treatment of an autoimmune disorder (e.g., lupus erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological wartare. An immunospenic CpG oligonuclectide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and Gaps conditions, and the infections which may be treated include viral, ö Score 8.4; DB 1; Length 12; Pred. No. 2.5e+02; 0; Mismatches 1; Indels Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:109. Sequence 12 BP; 0 A; 6 C; 1 G; 5 T; 0 U; 0 Other; Verthelyi D; Claim 4; Page 40; 46pp; English AAC80689 standard; DNA; 12 BP. L2-APR-2000; 2000WO-US009839 99US-0128898P. 32.3%; 90.06 14-FEB-2001 (first entry) 9; Conservative 18 1 TCGCCCTTTC 10 Klinman D, Ishii K, WPI; 2001-006880/01. (ISHI/) ISHII K. (VERT/) VERTHELYI D. 9 TCGCCCCTTC Query Match Best Local Similarity (KLIN/) KLINMAN D. (ISHI/) ISHII K. WO200061151-A2. 12-APR-1999; 19-OCT-2000. Synthetic. AAC80689; RESULT 457 Matches AAC80689 856666666666665558 ð 셤

CC comprise one of the generic sequences 5'-NNNN-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
C optionally have phosphorotrohicate linkages which make them more resistant
CC degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
C agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cellCC delivery complex. The oligonucleotides are able to induce either a cellCC cligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-RNNT-CpG-WNNN-3'
CC demin able to induce a humoral response. It is thought that after
CC demin able to induce a munoral response. It is thought that after
CC demin able to induce a munoral response is useful for reating presenting cells
CC demin able to induce an uncour by activation of T- or B-cells. The
CC demin and loration of matural killer (NK) cells. A cell-mediated or
CC induction of an immune response is useful for treating preventing or
Where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC conditions, and the infections which may be treated include eczema, allergic
CC conditions, and the infections which may be treated include viral,
CC conditions, and the infections which may be treated include viral,
CC conditions, and the infections which may be treated include viral,
CC conditions, and the infections which may be treated include or a long or
CC condition and schistosomiaais. Immune response induction may also be
CC deshmania and schistosomiaais. Immune response induction may also be
CC deshmania and schistosomiaais. Immune response induction of an immune response is useful for treating solid tumour cancer. The induction of an immune celluin and signated and activated by manifered to immu lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CPG oligodeoxynucleotide of the invention

Sequence 12 BP; 0 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Gaps ; 0 32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; 1; Indels 0; Mismatches Query Match
Best Local Similarity 90.v.
9, Conservative 9 TCGCCCCTTC 18 ઠે

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ABI26159 standard; DNA; 12 BP. ABI26159; RESULT 458 ABI26159/ ID ABI2

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 326132 for detecting SNP TSC0032929.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 329062 for detecting SNP TSC0034738.
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                                                oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                      Claim 1; SEQ ID NO 326132; 29pp + Sequence Listing; German.
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 Berlin K;
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1es 9; Conservative
 Olek A, Piepenbrock C,
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                              WPI; 2001-657177/75.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 329062; 29pp + Sequence Listing; German. WPI; 2001-657177/75.

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Piepenbrock C,

olek A,

(EPIG-) EPIGENOMICS AG.

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2.

18-OCT-2001.

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              range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09988, ABC0010-ABE9988, ABH00010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 311066 for detecting SNP TSC0024292.
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                                                                                                                                                                                                                                              Query Match 32.3%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                   13 CCCTTCCTAA 22
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32.3%; Score 8.4; DB 1; Length 12;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                    Gaps
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                    Indels
   Pred. No. 2.5e+02;
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90.0%;
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90.08;
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                                           9; Conservative
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Best Local Similarity
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18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                               Oligonucleotide primer SEQ ID NO 370673 for detecting SNP TSC0058310.
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                22-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 362920; 29pp + Sequence Listing; German.
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                              06-APR-2001; 2001WO-IB000713.
                                                             07-APR-2000; 2000DE-01019173.
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                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                               Claim 1; SEQ ID NO 321695; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                               32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02;
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                        Oligonucleotide primer SEQ ID NO 347844 for detecting SNP TSC0045291.
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                                                       ABI47871 standard; DNA; 12 BP.
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                                                                             ABI47871;
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                                  RESULT 467
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a cange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                    Oligonucleotide primer SEQ ID NO 313066 for detecting SNP TSC0025454.
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                                                                                        Gaps
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                                          32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                               oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                             Claim 1; SEQ ID NO 378511; 29pp + Sequence Listing; German.
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABR00010-ABR99999, ABR00010-ABR99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fibe.bublished_pot_sequences
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                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                               Oligonucleotide primer SEQ ID NO 302282 for detecting SNP TSC0019906.
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                                                   (first entry)
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                                                                                                                                                                                          Homo sapiens
                                                   22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
            Oligonucleotide primer SEQ ID NO 288980 for detecting SNP TSC0013751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 342202 for detecting SNP TSC0004659.
                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 288980; 29pp + Sequence Listing; German.
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                                                                                 Homo sapiens
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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9; Conservative
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ABI69041 standard; DNA; 12 BP.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 369014 for detecting SNP TSC0057403.
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                 Claim 1; SEQ ID NO 349360; 29pp + Sequence Listing; German.
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                      Oligonucleotide primer SEQ ID NO 365082 for detecting SNP TSC0054906.
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                                  ABI65109 standard; DNA; 12 BP.
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ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99899, ABF00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                Claim 1; SEQ ID NO 326235; 29pp + Sequence Listing; German.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

Claim 1; SEQ ID NO 280793; 29pp + Sequence Listing; German.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

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and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                      Gaps
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Score 8.4; DB 1; Length 12;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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                                                                                                                      ABI09127 standard; DNA; 12 BP.
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Best Local Similarity 90.0
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ABI09127
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                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                      Oligonuclectide primer SEQ ID NO 284413 for detecting SNP TSC0011825.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                          Claim 1; SEQ ID NO 292008; 29pp + Sequence Listing; German.
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 349177 for detecting SNP TSC0045956.
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                                                                                                                                                                     Query Match 32.3%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                Sequence 12 BP; 1 A; 1 C; 10 G; 0 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 356644 for detecting SNP TSC0006722.
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designed to detect single-nucleotide polymorphisms and cytosine
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ABI71473 standard; DNA; 12
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(EPIG-) EPIGENOMICS AG
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 9; Conservative
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                                                                                    Homo sapiens
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, and not also used for detecting cell type differentiation. ABC0011 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                 Claim 1; SEQ ID NO 359168; 29pp + Sequence Listing; German.
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07-APR-2000; 2000DE-01019173
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                                                                Piepenbrock C,
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                                 (EPIG-) EPIGENOMICS AG.
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               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but the was obtained in electronic format from WIPO at the printed specification, but firm wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                            Seguence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
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Best Local Similarity 90.v.
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                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 309969 for detecting SNP TSC0023756.
                                                                    Gaps
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                           Score 8.4; DB 1; Length 12;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences
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RESULT 501

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Olek A, Piepenbrock C, Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABR0010-ABH99989 and ABI0010-ABH9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent din oct form part of the printed specification, but
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                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                             Oligonucleotide primer SEQ ID NO 343432 for detecting SNP TSC0043069.
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         ABI43459 standard; DNA; 12 BP.
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aid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic
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                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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90.0%; Pred. No. 2.5e+02;
cive 0; Mismatches 1
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Best Local Similarity 90.0
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 318251 for detecting SNP TSC0028539.
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                                                                                                                                                                                                                                                                                                                                              32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02;
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ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                 Oligonucleotide primer SEQ ID NO 332009 for detecting SNP TSC003653B.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE099899, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Oligonucleotide primer SEQ ID NO 312863 for detecting SNP TSC0025339. of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine ; 0 Claim 1; SEQ ID NO 285723; 29pp + Sequence Listing; German. Claim 1; SEQ ID NO 312863; 29pp + Sequence Listing; German. Length 12; 1; Indels Seguence 12 BP; 1 A; 1 C; 6 G; 4 T; 0 U; 0 Other; 32.3%; Score 8.4; DB 1; 90.0%; Pred. No. 2.5e+02; 0; Mismatches ftp.wipo.int/pub/published_pct_sequences Berlin K; BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. ABI12890 standard; DNA; 12 (first entry) 9; Conservative Piepenbrock C, 1 CCACCTCATC 10 (EPIG-) EPIGENOMICS AG ~ 11 CCACCACATC WPI; 2001-657177/75. Local Similarity methylation status. methylation status. WO200177384-A2 Homo sapiens. 18-OCT-2001. 22-FEB-2002 ABI12890; Query Match Olek A, Matches ABI12890 RESULT 8 g

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ABI14794 standard; DNA; 12
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coligomers are also used for detecting cell type differentiation. ABC00010 aABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                           Oligonucleotide primer SEQ ID NO 314767 for detecting SNP TSC0026548.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Berlin K;
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Piepenbrock C,
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WPI; 2001-657177/75.
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                                                      Homo sapiens
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Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

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acid (PNA) oligomers for detecting single muclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99999, ABF00010-ABE99999, ABF0010-ABE99999 and ABI00010-ABE99999 and ABI00010-ABE90999 described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 2.5e+02;
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Best Local Similarity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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      32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
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Query Match 32.3
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Matches 9; Conservative
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                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                         Oligonucleotide primer SEQ ID NO 275065 for detecting SNP TSC0003772.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 330288; 29pp + Sequence Listing; German.
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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                                                              06-APR-2001; 2001WO-IB000713.
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WO200177384-A2.
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oligomers are also used for detecting cell type differentiation. ABC0001C-ABC9989, ABF00010-ABF99899, ABF00010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999 and ABF00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at first of the printed specification, but ftp.wipo.int/pub/published_pct_sequences

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 are present the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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ligonucleotides, useful for diagnosis and cell to detect single-nucleotide polymorphisms and
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Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

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Oligonucleotide primer SEQ ID NO 336857 for detecting SNP TSC0039556.
                                                                                                                      ABI36884 standard; DNA; 12
                                                                                                                                                                                          (first entry)
22
                                3 CCCTACCTAA 12
CCCTTCCTAA
                                                                                                                                                                                           22-FEB-2002
13
                                                                                                                                                         ABI36884;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 316873 for detecting SNP TSC0027651.

(first entry)

22-FEB-2002

ABI16900;

BP.

1900/c ABI16900 standard; DNA; 12

ABI16900,

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Berlin K; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 Piepenbrock C, (EPIG-) EPIGENOMICS AG. WO200177384-A2 Homo sapiens 18-OCT-2001 Olek A,

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine

designed to detect methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713

WO200177384-A2 Homo sapiens

18-OCT-2001.

Claim 1; SEQ ID NO 316873; 29pp + Sequence Listing; German

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 336857; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at Gaps ö 32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other; Best Local Similarity 90.0 Matches 9; Conservative Query Match

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Oligonucleotide primer SEQ ID NO 354713 for detecting SNP TSC0049238.
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                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                              ABI51216 standard; DNA; 12 BP.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coingomers are also used for acidovascular and metabolic disorders. The oligomers are also used for actiovascular and metabolic disorders. The represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                              (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 367153; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                          32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                         Gaps
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                                               32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
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                        Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 289742 for detecting SNP TSC0014077.
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ABH89749 standard; DNA; 12
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but the was obtained in electronic format from WIPPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                            Claim 1; SEQ ID NO 364671; 29pp + Sequence Listing; German.
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Best Local Similarity 90.00,
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                            range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ADC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF99989, ABF00010-ABF99999, ABF000010-ABF99999, ABF00010-ABF99999, ABF000010-ABF99999, ABF000010-ABF99999, ABF000010-ABF99999, ABF000010-ABF999999, ABF000010-ABF999999, ABF000010-ABF999999, ABF000010-ABF99
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oligonucleotides are used for diagnosis and/or prognosis of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 324837 for detecting SNP TSC0032252.
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32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 328462 for detecting SNP TSC0034314.
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                  Indels
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Pred. No. 2.5e+02;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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                                               CCACCTCATC 10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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ABI04927/c
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a renge of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                  Oligonucleotide primer SEQ ID NO 304900 for detecting SNP TSC0021161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 330664 for detecting SNP TSC0035645.
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                 22-FEB-2002 (first entry)
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Best Local Similarity 90.07
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 330664; 29pp + Sequence Listing; German.
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                              06-APR-2001; 2001WO-IB000713.
                                                               07-APR-2000; 2000DE-01019173.
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1es 9; Conservative
                                                                                                                              Olek A, Piepenbrock C,
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                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancer also used for advanced in gastrointestinal, respiratory, oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                         Claim 1; SEQ ID NO 335478; 29pp + Sequence Listing; German
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                    methylation status.
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represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                   Score 8.4; DB 1; Length 12; Pred. No. 2.5e+02;
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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CCCTTCATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Bust Local Similarity 90.00,
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                                                                  Homo sapiens
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                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
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                                                                                           set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshie methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers as also used for detecting cell type differentiation. ABC00010-ABE09989, ABF00010-ABE99989, ABH00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formm part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                          32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; ative 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 342960 for detecting SNP TSC0042805.
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                                              of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                      Claim 1; SEQ ID NO 290023; 29pp + Sequence Listing; German.
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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90.0%;
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Best Local Similarity
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                                                                      designed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                  06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides,
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC09989, ABR00010-ABR99899, ABR00010-ABR99899 and ABI00010-ABR80973 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ffp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                         Score 8.4; DB 1; Length 12;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a cange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989, ABF00010-ABH99989, ABF00010-ABH99989, ABF00010-ABH99989, and ABIO0010-ABH99980, represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 362857 for detecting SNP TSC0053491.
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                             3 TCCTAAACAT 12
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peptide nucleic
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ABI67081/c
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Query Match 32.3%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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            Oligonucleotide primer SEQ ID NO 367054 for detecting SNP TSC0056123.
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                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 367054; 29pp + Sequence Listing; German.
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                                                                                 Homo sapiens
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 275066 for detecting SNP TSC0003772.
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                                                                                                                                                                                                                                                                  designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                          German.
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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90.0%;
06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 90...
Best Some 9; Conservative
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ABI26346 standard; DNA; 12 BP.
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                                                                              Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI83073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 328868 for detecting SNP TSC0034609.
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                                                                                                                        Query Match 32.3%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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was obtained in electronic format from WIPO ftp.wipo.int/pub/published_pct_sequences
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                                                 This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disponsis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, callomers are also used for detecting cell type differentiation. ABC00010 and passent the oligomers described in the invention. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but we obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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       Claim 1; SEQ ID NO 275066; 29pp + Sequence Listing; German.
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Query Match
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                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                       Oligonucleotide primer SEQ ID NO 285720 for detecting SNP TSC0012410.
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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                                ABH85727 standard; DNA; 12 BP.
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                     Homo sapiens.
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Berlin K;

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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
      Piepenbrock
                 WPI; 2001-657177/75
                                         methylation status.
     Olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disquosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99989, ABF00010-ABF99989, ABH00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Claim 1; SEQ ID NO 316733; 29pp + Sequence Listing; German. 32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences Query Match
Best Local Similarity 90.v.
9, Conservative CITCCIAAGC 24 12

CTTCCTAACC 11 N ð a

ABI45290 standard; DNA; 12 BP. 22-FEB-2002 ABI45290; RESULT 560 ABI45290/

Oligonucleotide primer SEQ ID NO 345263 for detecting SNP TSC0043938. (first entry) CCXSXLTLLXBXBXBXBXBXBXBXSXXXXXXBXCCCX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 345263; 29pp + Sequence Listing; German.

nucleic This invention describes novel oligonucleotide primers or peptide nuclei acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9998 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences 888888888888888

Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Gaps ö 32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; Live 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0%, 22 N CCCTTCCTAA CACTTCCTAA 13 ò 셤

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RESULT 561

ABI63784 standard; DNA; 12 ABI63784; AB163784

BP.

(first entry) 22-FEB-2002

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Gaps

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 363757 for detecting SNP TSC0054044.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin Olek A, Piepenbrock C,

Ϋ.

WPI; 2001-657177/75.

78 Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 363757; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a reange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABH99989 and ABIO0010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 2 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

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                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Length 12;
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Score 8.4; DB 1;
Pred. No. 2.5e+02;
0; Mismatches 1;
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Similarity 90.0%;
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ABI21890 standard; DNA; 12 BP.

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                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                       Oligonucleotide primer SEQ ID NO 321863 for detecting SNP TSC0030535.
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22-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABR00010-ABB99999 and ABI00010-ABB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two was obtained in electronic format from WIPO at
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                                                                                                                                            Berlin K;
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                                                                                                                                        Piepenbrock C,
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                                                                                                         (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABIE2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                         Claim 1; SEQ ID NO 275539; 29pp + Sequence Listing; German.
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                                      methylation status,
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                        32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
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                                                                                                                     Sequence 12 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99999, ABF0010-ABE99999 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated ganomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010, ABC99999, ABF00010-ABF9999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fitp.wipo.int/pub/published_pct_sequences
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899 and ABI00010-ABF2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclocides are used for disagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI001010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but the wipo.int/pub/published_pct_sequences
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                        This invention describes novel oligonucleotide primers or peptide nucleic
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                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                  Oligonucleotide primer SEQ ID NO 375415 for detecting SNP TSC0061236.
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                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                            set or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                     Claim 1; SEQ ID NO 298623; 29pp + Sequence Listing; German.
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Matches 9; Conservative
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            WPI; 2001-657177/75
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                          central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF9989, ABH00010-ABH99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
gastrointestinal, respiratory,
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range of diseases including immune system,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC99899, ABF00010-ABE99899, ABH00010-ABH99989 and ABI000110-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                 Oligonucleotide primer SEQ ID NO 348872 for detecting SNP TSC0045798.
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      22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 345264 for detecting SNP TSC0043938.
         Gaps
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                                          TTCCTAAGCA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 358795 for detecting SNP TSC0051310.
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ftp.wipo.int/pub/published_pct_sequences
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                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                     Claim 1; SEQ ID NO 358795; 29pp + Sequence Listing; German.
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methylation status.
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ABH79604 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                            Gaps
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                                                                                                    32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02;
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                                                                     Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms trom WIPO at
                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                            Oligonucleotide primer SEQ ID NO 279597 for detecting SNP TSC0007579.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coligomers are also used for detecting cell type differentiation. ABC00010 oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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      Length 12;
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                                                                     1; Indels
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   32.3%; Score 8.4; DB 1;
90.0%; Pred. No. 2.5e+02;
iive 0; Mismatches 1;
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Query Match 32.3
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                              17 TCCTAAGCAT
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ABH93554/c
ID ABH935
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WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                          Oligonucleotide primer SEQ ID NO 293547 for detecting SNP TSC0015665.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                        WO200177384-A2
                                                                                                                                 Homo sapiens
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and
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Best Local Similarity
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF0010-ABF9989, ABH0010-ABH99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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tive 0; Mismatches 1;
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Oligonucleotide primer SEQ ID NO 345058 for detecting SNP TSC0043853.
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                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Wed May 10 10:49:52 2006

Berlin K;

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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                        Claim 1; SEQ ID NO 371774; 29pp + Sequence Listing; German.
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        07-APR-2000; 2000DE-01019173,
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 359359; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 90.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 CCCCTTCCTA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 CTCCTTCCTA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2002
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  & X C C C C C C C C C X S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, caignment are also used for acidovascular and metabolic disorders. The oligomers are also used for actecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 and actabolic disorders did not form part of the printed specification, but the was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 359359 for detecting SNP TSC0005314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; ative 0; Mismatches 1; Indels
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Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

BP.

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ACC83136 standard; DNA; 12
                                 ACC83136;
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  ACC83136
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                                                                                                                                                                                                                                                            CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of CpG oligodeoxynucleotide DV137 of the invention. A claimed method for generating dendritic cells involves concacting a dendritic cell precursor, especially a monocyte, with a D type oligodeoxynucleotide (see ACC48294) containing a central unmethylated CpG motif. The method is useful for generating mature persentation. Mature dendritic cells are useful for tumour immunotherapy, for augmenting an immune response to an infectious agent or to a vaccine, and as vaccines to prevent future infection or to activate the immune system to treat diseases such as cancer. Mature dendritic cells may also be used to produce activated I lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                  Gaps
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                                          Query Match 32.3%; Score 8.4; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 2.5e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 BP; 0 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
                      Sequence 12 BP; 3 A; 5 C; 0 G; 3 T; 0 U; 1 Other;
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                Verthelyi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 8; 69pp; English.
                                                                                                                                                                                                                                     CpG oligodeoxynucleotide DV137.
                                                                                                                                                                     ACC48331 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                              13-AUG-2002; 2002WO-US025732.
                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2001; 2001US-0312190P
                                                                                                                                                                                                                (first entry)
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                                                                                        15 CTTCCTAAGCA 25
                                                                                                            CTTCNTAACCA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-300874/29.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                  WO2003020884-A2.
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                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                          ACC48331;
                                                                                                                                               RESULT 601
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                                                                                                                                                           ACC48331
                                                                                                                                                                      SXS
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The invention relates to sterically stabilised cationic liposomes (SSCL) which comprises a cationic lipid, a co-lipid, stabilising agent and comparises a cationic lipid, a co-lipid, stabilising agent and companiation is useful in pharmacettical composition for impairing composition is expression of a cytokine (e.g. human tumour cell) bearing an immune response, which is expression of a cytokine (e.g. interferon gamma), particularly immunotherapeutic response against tumours or stimulating an in vivo or an in vitro immune cell, and for inducing an immune response against an infectious agent e.g. virus, bacteria and fungus. It is also useful for an infectious agent e.g. virus, bacteria and fungus. It is also useful for delivering oligodeoxynuclecides including a CpG motif in clinical applications; for treating infectious diseases (e.g. tularemia, malaria, for applications, allergy (e.g. eczema, allergic rhinitis or coryza, hay fever, cetc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever, cetc), allergic asthma, utticaria, food allergies), autoimmune cetcomianially and psoriasis. The present sequence is a D class CpG con potentially useful for encapsulating in SSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                    Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic liposome composition for delivering oligodeoxynucleotides including a CpG motif in clinical applications, comprises a cationic lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
                                                                                                                                                                                                   tuberculosis, cytokine, leishmaniasis, AIDS-associated Kaposi's tumour;
thyroid, cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
schistosomiasis, interferon gamma; lupus erythematosus; antimicrobial;
asthma; urticaria; autoimmune diameatis, diabetes; heumatoid arthritis;
cpg motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Puri RK;
                                                                               D class CpG ODN sequence useful for encapsulating in SSCL, DV137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Joshi BH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 12 BP; 0 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii KJ, Kawakami K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            multiple sclerosis; infection; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 10C; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-2002; 2002WO-US024235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-2001; 2001US-0308283P.
25-JUL-2002; 2002US-00206407.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klinman DM, Gursel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003040308-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
27-AUG-2003
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RESULT 603

TCGCCCCTTC 18 ||||| || |||| TCGCCGCTTC 10

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RESULT 602

ADD01112

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Inducing the production of vascular endothelial growth factor by a cell, useful for inducing angiogenesis, comprises contacting the cell with a CPG oligodeoxynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis or ischaemia. The method may also be used in screening for agents that inhibit neovascularisation. The present sequence represents a CPG oligonucleotide which is used in the exemplification of
                                                                               neovascularisation, angiogenesis, vulnerary, vasotropic;
antiarteriosclerotic, gene therapy, skin graft, male pattern baldness;
atherosclerosis; ischaemia; ss.
                                                                      vascular endothelial growth factor; VEGF; CpG oligonucleotide;
                                                                                                                                                                                                         (UYTE-) UNIV TENNESSEE RES CORP.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                           Example 7; SEQ ID NO 76; 37pp; English.
                                                     CpG K oligonucleotide SEQ ID NO:76.
 BP
                                                                                                                                                                      19-DEC-2002; 2002WO-US040955.
                                                                                                                                                                                         20-DEC-2001; 2001US-0343457P.
ADD01112 standard; DNA; 12
                                   (first entry)
                                                                                                                                                                                                                                   Klinman DM, Zheng M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention.
                                                                                                                                                                                                                                                      WPI; 2003-559138/52.
                                                                                                                                   WO2003054161-A2.
                                   01-JAN-2004
                                                                                                                                                     03-JUL-2003
                                                                                                                  Synthetic.
                 ADD01112;
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                                 32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
Sequence 12 BP; 0 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
                                                                  9; Conservative
                             Query Match
Best Local Similarity
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Matches
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9 TCGCCCCTTC
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ABZ72905/c RESULT 604

ABZ72905 standard; RNA; 12 BP.

(first entry) 09-APR-2003

Rod opsin hammerhead ribozyme oligonucleotide.

ophthalmological; gene therapy; eye; retinal dysfunction; AAV; diabetic retinopathy; macular degeneration; autosomal dominant retinitis; blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss. Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

Synthetic

Homo sapiens.

WO200288320-A2.

07-NOV-2002.

01-MAY-2002; 2002WO-US013679.

(UYFL) UNIV FLORIDA

01-MAY-2001; 2001US-00847601.

Grant MB; Shaw LC, Lewin AS,

WPI; 2003-111880/10.

useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular A recombinant adeno-associated virus-vectored ribozyme composition, degeneration.

Example 5; Page 66; 115pp; English.

The present librarion describes a recombonant acenomesociated virus present librarion describes a recombonant acenomesociated virus present librarion describes a recombonant acenomesocial at least a first ribozyme that specifically cleaves an mRNA encoding a protein, collaborate or peptide selected from the group of rod opsin, iNOS.

RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha 1, integrin alpha 6, or integrin alpha 7, integrin alpha 7, or integrin alpha 1, integrin alpha 1, integrin alpha 3, integrin alpha 6, or integrin alpha 1, integrin alpha 1, integrin alpha 1, integrin alpha 1, integrin alpha 3, integrin alpha 6, or integrin alpha 1, integrin alpha 1, integrin alpha 3, integrin alpha 6, or integrin alpha 1, integrin alpha 1, integrin alpha 3, integrin alpha 6, or integrin alpha 1, integrin alpha 1, integrin alpha 3, integrin alpha 2, or integrin alpha 1, integrin alpha 2, integrin and 2, integrin and 2, integrin and 2, integrin and 2, integrin alpha 2, integrin alpha 2, integrin and 2, integrin and 2, integrin alpha 2, integrin and 2, integrin alpha 2, integrin and 2, integrin and 2, integrin alpha 2, integrin alpha 2, integrin alpha 2, integrin alpha 2, inte present invention describes a recombinant adeno-associated virus exemplification of the present invention

Sequence 12 BP; 4 A; 2 C; 5 G; 0 T; 1 U; 0 Other;

.. 0 32.3%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.5e+02; 1; Indels 0; Mismatches 9; Conservative Query Match Best Local Similarity Matches

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Gaps

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15 CTTCCTAAGC 24

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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
         09-OCT-1992;
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19-JUN-1998;
19-JUN-1998;
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19-JUN-1998;
19-JUN-1998;
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                                                                                                                                                                                                                                                                         AAZ79009;
                                                                  reaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; PCR; amplify; primer; differentiation; rice; Oryza sativa; electrophoresis; ss.
                                                                                                                                                                                                                                                                                               The sequences given in AAQ65443-50 are primers which were used in the differentiation of lettuce, Lactuca sativa, by multiplication of its genome. The amplification products are electrophoresed to allow separation, and differences noted. These primers were produced by standard methods of solid phase synthesis
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                         - by
                                                                                                                Polymerase chain reaction; primer; amplify; PCR; differentiation; lettuce; Lactuca sativa; electrophoresis; ss.
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0
                                                                                                                                                                                                                                                         Differentiation of lettuce species using oligo-nucleotide(s)
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                               30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                Lactuca sativa differentiation primer (1).

 Bativa differentiation primer (1).

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                                               AAQ65443 standard; DNA; 10 BP.
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                                                                                                                                                                                        92JP-00271759
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                                                                                (first entry)
                                                                                                                                                                                                                                                                 polymerase chain reaction.
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Best Local Similarity 100.
Matches 8; Conservative
TCCTAAGC 24
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                                                                                                                                                  Differentiation of rice species using oligo-nucleotide - by polymerase
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                                                                                                                                                                                                                           Claim 1; Page 2; 15pp; Japanese
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                                                                                                   WPI; 1994-172748/21
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SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; moncoyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CLL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                        Human dendritic cell SAGE tag, SEQ ID NO:678.
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                                                                                                             WO9965924-A2,
                                                                                                                                 Homo sapiens
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           Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be correspond to novel genes. Attigen-presenting cells (expressed sequence tags) which were previously unknown to be correspond to novel genes. Attigen-presenting cell correspond to novel genes. Attigen-presenting cell corpitation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly companies to modulate the genotype of an APC; to screen to an APC; and as hybridisation probes/amplification primers for the diagnosis and monitoring of diseases related to abnormal companies of these genes. Detection of the dendritic cell differentially expressed genes in expressed genes, or of their encoded proteins, can be used in active immunotherapy. Co-administration of tumour antigens and population of antigen-specific effector cells) and vectors containing these companies appearance antigen and processed dequate a
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                                                                                                                                                                                                                                                                                  cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                                                                                                               Claim 1; Page 106; 130pp; English
                              98US-0090076F.
98US-0090077P.
98US-0090078P.
98US-0090079P.
98US-0090080P.
   98US-0090048P.
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                                                                           19-JUN-1998;
19-JUN-1998;
08-DEC-1998;
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(SHAN/)
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98US-0089992P. 98US-0089993P. 98US-0089994P. 98US-0089997P. 98US-0090000P.

98US-0090040P. 98US-0090036P.

98US-0090042P.

98US-0090045P 98US-0090048P

98US-0090076P 98US-0090077P 98US-0090078P 98US-0111715P

98US-0090044P

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Sequences AA277573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while cother transcripts correspond to novel genes. Antigen-presenting cell cother transcripts correspond to novel genes. Antigen-presenting cell cother transcripts orrespond to novel genes. Antigen-presenting cell cother transcripts orrespond to novel genes. Antigen-presenting cell cother transcripts antigen presentation via the MRC (major histocompatibility cells. Tumour antigen presentation via the MRC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytocoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for
                                                                                                                                    Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 84; 130pp; English.
WPI; 2000-106077/09.
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Gaps

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2.9e+02;

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Matches

CCACCTCA 10

AAZ78250 standard; DNA; 10 BP.

AAZ78250;

10-APR-2000 (first entry)

98US-0090047P

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efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expressed genes. Detection of the dendritic cell differentially expressed genes. Detection of the dendritic cell differentially captessed genes, or of thair encoded proceins, can be used to identify calls as belonging to the moncoyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a popularion of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation of co-stimulatory signals, migration to T cell-rich sites, recruitment of immune effector cells
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98US-0089993P.
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Expression) tags used to identify mRNA transcripts encoding composed to identify mRNA transcripts encoding composed to identify mRNA transcripts encoding composed in monocyte-derived dendritic cells compared differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while content transcripts correspond to novel genes. Antigen-presenting cell cativation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour antigen presentation of cytotoxic immune response that can lyse the tumour antigen, immunostimulatory cofactors also being required for cfficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGB tags have several potential uses.

They may be used in vaccines to induce an immune response, particularly capanist a tumour antigen, to modulate the genotype of an APC; to screen cfor against a tumour antigen, probes/amplification primers for the approssion of these genes in complex and monitoring of diseases related to abnormal corpusation of these genes. Detection of the dendritic call differentially expressed genes, or of their encoded proteins, can be used on active immunotherapy (or to stimulate production of active immunotherapy (or to stimulate production of them are used in active immunotherapy (or to stimulate production of them are used in active immunotherapy. Co-administration of containing these genes corpused presentation of co-stimulatory signals, migration of chemospace of the measurement
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100.0%; Pred. No. 2.9
:ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Sequences AA277573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC) associated costimulatory factors play an important role in the activation of the cytocoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MMC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse
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                                                   SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                          Human dendritic cell SAGE tag, SEQ ID NO:1041.
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the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid sequences identified using the SAGE tags have several potential uses.

They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen car an about the modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal carperssed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a copulation of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen correspondent of co-stimulatory signals, migration to T cell srowth factors and secretion of chemokines for recruitment of immune effector cells
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                                                               AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metaatatic breast tumour clissum (1.e. are upregulated in metaatatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour clissum (1.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, monitoring and transcripts can be used for diagnosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of particularly an antigen encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic capnits. Host cells that produce the polypeptides or as therapeutic capnits. Host cells that produce the polypeptides or as therapeutic capnits. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antipen-specific immune effecter immune effecter immune the capnity immune the cells immune the capnity immune the capnity immune immune the capnity immune immune
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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                                    Claim 1; Page 131; 219pp; English.
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 treatment of cancer.
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(ROBE/)
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour citises (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour citises (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, monitoring and transcripts can be used for diagnosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of cell therapeutic genes (also riboxymes or antisense sequences).

Compounds that modulate expression of the transcripts are also useful in particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific or antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immune effecter immune effecter.
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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                   Claim 1; Page 121; 219pp; English.
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                                                       treatment of cancer.
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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AAZ83873;
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                                                                                             that are preferentially transcribed in the metastatic breast tumour that are preferentially transcribed in the metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, monitoring and transcripts can be used for diagnosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).

Compounds that antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-egecific immune effecter cells.
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                        Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                         Claim 1; Page 174; 219pp; English.
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SHANKARA S.
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that are preferentially transcribed in the metastatic breast tumour cells). AAZ80767 to AAZ80341 represent tags corresponding to distinct transcripts that are preferentially transcribed in metastatic breast tumour cells). AAZ80342 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downrequlated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).

CC particularly a manigane-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antispense sea be used to expand and isolate populations of educated, antispense used for adoptive cells.
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Roberts BL, Shankara S;
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Best Local Similarity
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Roberts BL, Shankara S;

WPI; 2000-106079/09.

(GENZ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.

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that are preferentially transcribed in the metaatatic breast tumour that are preferentially transcribed in the metaatatic breast tumour cells). AZB3942 tissue (i.e. are upregulated in metaatatic breast tumour cells). AAZB3942 to AAZB6677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour citsue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts are potentially where metaatatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).

Compounds that modulate expression of the transcripts are also useful in particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic capnis sequences. Cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
                                                                                                                  Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 30.8%; Score 8; DB 1; Length 10; Local Similarity 100.0%; Pred. No. 2.9e+02; les 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                               Claim 1; Page 142; 219pp; English.
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98US-0089997P.
98US-0090039P.
98US-0090040P.
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                                       Roberts BL, Shankara S;
                                                                                                                                                            treatment of cancer.
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(SHAN/) SHANKARA S.
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19-JUN-1998;
19-JUN-1998;
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour cells). AAZ83942 tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downrequlated in metastatic breast tumour cells). These transcripts can be used for diagnosis, monitoring and transcripts can be used for diagnosis, monitoring and treatment of breast cancer, particularly where metastatic Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).

Compounds that modulate expression of the transcripts are also useful in particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific or antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic capnits. Host cells that produce the polypeptides or as therapeutic cells.
                                                                                                                                           Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                    Claim 1; Page 178; 219pp; English.
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98US-0089997P.
98US-0090039P.
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                                                                                                                                                                                   treatment of cancer.
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19-JUN-1998;
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99JP-00095481
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            19-JUN-1998;
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AAC74102/c
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                                                                                                                                                                                                   that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upreglated in metastatic breast tumour cells). AAZ89342 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in metastatic breast tumour cells). AAZ863342 to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and transcribts can be used for diagnosis, prognosis, monitoring and creatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoaspays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter.
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                                                                                                                            Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                Claim 1; Page 202; 219pp; English.
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98US-0090041P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                            Shankara S;
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                        (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                                                                       treatment of cancer.
                                                                                                    WPI; 2000-106079/09
                                                 SHAN/) SHANKARA S.
19-JUN-1998;
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                                                                            Roberts BL,
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Matches
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that are preferentially transcribed in the metastatic breast tumour cells). AAZ80767 to AAZ80341 represent tags corresponding to distinct transcripts that are preferentially transcribed in metastatic breast tumour cells). AAZ8042 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific transcribes are used to detect the polypeptides or as therapeutic genes. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic genes. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immune effecter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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autoimmune disease; tumour; ss.
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100.0%; Pred. No. 2.9
:ive 0; Mismatches
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98US-0090040P.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer.
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Performing differential display of prokaryotic mRNA by a RT (reverse transcriptase)/RAP (random arbitary-primed) PCR based technique comprises using a unique combination of random primers in a single amplification
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                                                                                           Claim 10; Page 13; 95pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                  Prokaryote RT-PCR primer PCR10.
                                                                                                                                                                                                                                                                                                                                                        AAA99868 standard; DNA; 10 BP.
                         Hashimoto S, Matsushima K,
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                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                           and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                          (revised)
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                                         WPI; 2000-619172/59
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                                                                           disease and tumors.
                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200056936-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-2003
26-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley WE,
                                                                                                                                                                                                                                                                                                                                                                         AAA99868;
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria
                                                                                                                                                                                                                                                                                                                                       RESULT 622
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                 AAA99868,
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of prokaryotic mRNA by RT-DCR. This involves the amplification of the mRNA once, and the further amplification of the crepeated amplification of the mRNA once, and the further amplification of the cDNA, rather than the repeated amplification of the mRNA sample. It also eliminates the need for sequencing gels, using Northern and total RNA dot blots to confirm differentially displayed transcription levels. The primers AAA99869-A99868 were used in a reverse transcription PCR amplification, and primers AAA99869-A99876 were used to prepare probes for a Northern blot analysis. The method can be used to rapidly identify genes with increased or decreased transcription following environmental stimuli, in bioprocess fermentations, and to analyse gene regulation. (Updated on 06-AUG-2003 to correct OS field.)
                                                            present invention is concerned with a method of differential display
                                                                                                                                                                                                                                                                                                                                                                        30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta-phaseolin promoter vicilin box site A motif.
                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
                   Claim 1; Page 19; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC84558 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
1es 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                        The present invention describes a group of genes consisting of 100 genes which are highly expressed in human dendritic cells; a group of genes which are expressed at a higher frequency in human dendritic cells than in human monocytes; and a group of genes which are expressed at lower frequency in human dendritic cells than in human monocytes. Each group of genes are characterised in that cDNAs of these genes respectively have the base sequences of SEQ ID NO:11 to 100 (AAC74014 to AAC74014). SEQ ID NO:101 to 200 (AAC74014 to AAC74013) and SEQ ID NO:201 to 300 (AAC74114) located most closely to the poly-A region. The sequence 5'-CATG-3' the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study and diagnosis of diseases in which dendritic cells play a significant role, e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                 Groups of genes expressed in human dendritic cells at a greater or lesser extent than in monocytes for investigation and diagnosis of autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
            (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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Gaps

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0; Indels

Transcription factor; seed storage protein; lectin; oil-body protein; Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; 7S-globulin; phaseolin; PHA-L; bean; nuclear protein; promoter; ds. The invention relates to an isolated transcription factor gene which is expressed in a recombinant maturing dicot seed and which encodes a transcription factor protein which targets a promoter of a gene encoding seed storage proteins, lectins or oil-body proteins. The transcription factors isolated are Pv-Seed factor-1 (ROM1) and Vicilin-box binding protein-1 (ROM2). These factors bind to 78-globulin (b-phaseolin) or lectin (PHA-L) promoters. The transcription factor gene is useful for enhancing or reducing expression of seed storage protein, lectin or oil-protein genes in dicot seed crops. The present sequence represents a Novel transcription factor gene which encodes transcription factor protein that targets promoters of genes encoding seed storage proteins are useful for modulating seed storage protein expression in dicot seed (UYMA-) UNIV MARYLAND BALTIMORE COUNTY. Example 3; Col 9; 67pp; English. 97US-00796899 94US-00319544 Bustos MM; WPI; 2001-079619/09. Phaseolus sp. 06-FEB-1997; 07-OCT-1994; US6160202-A. 12-DEC-2000. Chern M, crops.

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Bustos MM;
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-079619/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCACCTCA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                  06-FEB-1997;
                                                                                                                                                                                                                                                                           07-OCT-1994;
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                                                                                                                                                                          Phaseolus sp.
                                                                        02-APR-2001
                                                                                                                                                                                                   US6160202-A.
                                                                                                                                                                                                                          12-DEC-2000.
                                                                                                                                                                                                                                                                                                                           Chern M,
                                                  AAC84562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH32689;
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 RESULT 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated transcription factor gene which is expressed in a recombinant maturing dicot seed and which encodes a transcription factor protein which targets a promoter of a gene encoding seed storage proteins, lectins or oil-body proteins. The transcription factors isolated are Pv-Seed factor-1 (ROM1) and Vicilin-box binding protein-1 (ROM2). These factors bind to 7S-globulin (b-phaseolin) or lectin (PHA-L) promoters. The transcription factor gene is useful for enhancing or reducing expression of seed storage protein, lectin or oil-protein genes in dicot seed crops. The present sequence represents a bean-lectin promoter (PHA-L) fragment to which ROM1 and ROM2 proteins bind to
                                                                                                                                                                                                                                                                                                 Transcription factor; seed storage protein; lectin; oil-body protein; Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; 7S-globulin; phaseolin; PHA-L; bean; nuclear protein; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel transcription factor gene which encodes transcription factor protein that targets promoters of genes encoding seed storage proteins are useful for modulating seed storage protein expression in dicot seed
delta-phaseolin promoter fragment (vicilin box site A motif) to which recombinant bZIP2 protein binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                            Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
                                    Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
                                                           Query Match
30.8%; Score 8; DB 1; Ler
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                           Bean lectin promoter PHA-L site C motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYMA-) UNIV MARYLAND BALTIMORE COUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Col 9-10; 67pp; English.
                                                                                                                                                                                                 AAC84563 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                          2 CCACCTCA 9
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Best Local Similarity
Matches 8; Conserv
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                                                                                                            1 CCACCTCA
                                                                                                                                                                                                                                                                                                                                                  Phaseolus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                            06-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                           US6160202-A.
                                                                                                                                                                                                                                                  02-APR-2001
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                                                                                                                                                                                                                          AAC84563;
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                                                                                                                                                                         RESULT 624
                                                                                                                                                                                       AAC84563
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                                                                                                                                                                                                                                    protein;
7S-globulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel transcription factor gene which encodes transcription factor protein that targets promoters of genes encoding seed storage proteins are useful for modulating seed storage protein expression in dicot seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST; expressed sequence tag; diagnosis; human disease; treatment; ss.
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                                                                                                                                                                                                                                 Transcription factor; seed storage protein; lectin; oil-body Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; phaseolin; PHA-L; bean; nuclear protein; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPS activated human monocyte expression gene cDNA tag SEQ:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 10; . 2.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 2.5
ive 0; Mismatches
                                                                                                                                                                          Bean lectin promoter PHA-L site B motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYMA-) UNIV MARYLAND BALTIMORE COUNTY.
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BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00319544.
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AAC84562 standard; DNA; 10
                                                                                                                  (first entry)
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Velculescu V, Vogelstein B, Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an lipopolysaccharide (LPS) activated human monocyte expression gene group consisting of the high-ranking 50 genes of the highest expression among the genes expressed by human monocyte stimulated by LPS in which the cDNA of each gene has the base sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-CATG-3' nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treatment of various human diseases in which human monocyte plays an important role. AAH33628 cxpAH32943 represent specifically claimed LPS activated human monocyte expression gene cDNA tags from the present invention. AAH3294 represents an LPS activated human monocyte axpression gene cDNA tags from the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast gene coding sequences comprising NORF genes with serial analysis
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SACB; serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11054.
                                                                                                                                                                                                                                                                                                                                      30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; ative 0; Mismatches 0; Indels
                                                                                                                                 LPS activated human monocyte expression gene group.
                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzler K;
                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                       Claim 10; Page 19; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF42915 standard; DNA; 10 BP.
                                                  28-APR-2000; 2000JP-00131079
                                                                       99JP-00195103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00335032
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100..
S. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linker; PCR primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                12 CCCCTTCC 19
                                                                                                                WPI; 2001-304369/32
                                                                                                                                                                                                                                                                                                                                                                                            CCCCTTCC 2
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         JP2001069993-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200077214-A2.
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                                                                      08-JUL-1999;
                             21-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 627
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cycle comprising administering a NORF gene whose expression varies by at phase, S phase and G2M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contribution much of a set substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human pones which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression of a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a cyeast cell comprising contacting a characteristic effect on gene expression in a cyeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell of at least 1 NORF gene whose cyeast contacting a yeast cell of at least 1 NORF gene whose cyeast cell comprising contacting a yeast cell cycle, the differentially expressed genes may be used to define an antifect phases of the cell cycle. The cycle and for identification of antifungal drugs. Aprimers used in the exemplification of the present invention.

Cycle and for identification of the present invention.
gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                         Example; Page 344; 419pp; English.
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.; 0 0; Indels DB 1; Length 10; 30.8%; Score 8; DB 1 100.0%; Pred. No. 2.9 Live 0; Mismatches Query Match Best Local Similarity 100.v.

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Gaps

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5039. AAF38300 standard; DNA; 10 BP. 23-MAR-2001 (first entry) AAF38300;

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; 14-JUN-2000; 2000WO-US016223 99US-00335032 (UYJO) UNIV JOHNS HOPKINS. Saccharomyces cerevisiae linker, PCR primer, ds. WO200077214-A2. 16-JUN-1999; 21-DEC-2000,

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, 5 phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF genes may be used as markers of phases of the cell cycle. The expressed genes may be used as markers of phases of the cell cycle. The cycle and for identification of antifungal drugs. AAF93268 to AAF44064 represent SAGE tags used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                       Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              method, in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                             Example; Page 180; 419pp; English.
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WPI; 2001-061874/07.
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Best Local Similarity
Matches 8; Conserv
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AAF40343/c
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cutifungal drugs comprising: (a) contexting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying under contacting human genes which are involved in cell cycle progression of contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a norm cell comprising contacting a yeast cell with a candidate drug and contacting expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially contacting expression in the yeast cell of at least 1 NORF gene may be used to identify candidate drugs which affect the cell cycle and feet phases of the cell cycle, the differentially cyclestes and for identification of antifungal drugs which affect the cycle and feet identify candidate drugs which affect the cycle and feet identification of antifungal drugs which affect the cycle method, in the exemplification of the present invention. Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Gaps Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. .; 0 0; Indels 30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9140. Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other; Jelculescu V, Vogelstein B, Kinzler K; Example; Page 252; 419pp; English AAF42401 standard; DNA; 10 BP. 14-JUN-2000; 2000WO-US016223 23-MAR-2001 (first entry) Query Match 30.8 Best Local Similarity 100. Matches 8; Conservative Saccharomyces cerevisiae. 18 CCTAAGCA 25 WPI; 2001-061874/07. 10 CCTAAGCA 3 WO200077214-A2. 21-DEC-2000. AAF42401; RESULT 630 **AAF4240**3 g ò

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analygis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering a NORF gene whose expression varies by at cycle comprising administering a NORF gene whose expression varies by at phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for ovaries as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contiguous nucleotides of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell own contacting a yeast cell with a candidate drug as (5) and (4) a method (M4) for identifying a claracteristic effect on gene expression in a cyeast cell own contacting a yeast cell with a candidate drug and yeast cell own contacting a peace of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The ceptressed genes may be used as markers of phases of the cell cycle. The ceptressed genes may be used to identify candidate drugs which affect the cell cycle and for identify candidate drugs. Which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and evel drugs represent linkers and evel phases of the cell cycle and evel the represent 
                                                                                                                                                                                                                                Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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Pred. No. 2.9e+02;
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Best Local Similarity 100.0%; Pred. No. 2.9
Matches 8; Conservative 0; Mismatches
                                                                                                                 Velculescu V, Vogelstein B, Kinzler K;
                                                                                                                                                                                                                                                                                                                                               Example; Page 326; 419pp; English
  99US-00335032
                                                        (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                       WPI; 2001-061874/07.
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  16-JUN-1999;
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RESULT 631

AAF36961 standard; DNA; 10 BP

(first entry) 23-MAR-2001

AAF36961;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3700.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonamnotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US016223

16-JUN-1999;

SNIXAOH SNHOC VINU (OCYU)

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 132; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate on tifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting are involved in cell cycle progression contiguous nucleotides of a NORP gene whose expression in a configuous nucleotides of a NORP gene whose expression in a configuous nucleotides of a NORP gene whose expression in the yeast cell with a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cyeast cell of at least 1 NORF gene whose cyeast cell comprising contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell of at least 1 NORP gene whose contoring expression in the yeast cell of at least 1 NORP gene whose contoring expression in the yeast cell of at least 1 Cycle. The expressed genes may be used as markers of phases of the cell cycle and for identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs which a present invention.

Cycle and for identification of the present invention of the pr

Sequence 10 BP; 4 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

0; Gaps

Gaps ö 30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; Live 0; Mismatches 0; Indels Best Local Similarity 100. Matches 8; Conservative Query Match

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15 CTTCCTAA 22 CTTCCTAA 10 m

ઠે g AAF43780,

AAF43780 standard; DNA; 10 BP. 23-MAR-2001 (first entry) AAF43780;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11919.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification, linker; PCR primer; ds.

Saccharomyces cerevisiae

Kinzler K;

Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

(UYJO) UNIV JOHNS HOPKINS

14-JUN-2000; 2000WO-US016223.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

99US-00335032

16-JUN-1999;

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonanotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cantifungal drugs comprising: (a) contacting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a comprising contacting a yeast cell with a candidate drug and conticoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene may be used to suppression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The cycles may be used to identify candidate drugs which affect the cell cycle and feet phases of the cell cycle and feet the charge subsidered by the class of the cell cycle and feet the charge subsidered by the examplification of the present invention. AAF31262 to AAF31367 represent linkers and the present invention.
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                                                                                                                                                                                                                                                                                                                      Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                                  Kinzler K;
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                                                                                          14-JUN-2000; 2000WO-US016223.
                                                                                                                                       99US-00335032
                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS.
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Best Local Similarity
Matches 8; Conservat
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WO200077214-A2.
                                                                                                                                       16-JUN-1999;
                                               21-DEC-2000
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cantifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotidate of a north a probe which comprises as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contiguous nucleotidate of a NORF gene whose expression is affected by the class of drugs. The NORF gene whose expression is affected by the class of the cell cycle, the differentially contacting expression in the yeast cell wige. And and fidert phases of the cell cycle in the expension of antifungal drugs which affect the cycle and for identification of antifungal drugs. The NORF genes may be used to identify candidate drugs which affect the cycle and for identification of antifungal drugs. The NORF present invention. AAF33261 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                             Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SACE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 365; 419pp; English.
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Best Local Similarity
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AAF37421
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Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11675.

nor previously assigned open reading frame; nonannotated ORF; SAGB; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

Kinzler K;

99US-00335032

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                             Example; Page 148; 419pp; English.
                                                   14-JUN-2000; 2000WO-US016223
                                                                                  Velculescu V, Vogelstein B,
                                                                        SNING OUTU ( OLYU)
                                                                                             WPI; 2001-061874/07.
                               WO200077214-A2
                                                              16-JUN-1999;
                                         21-DEC-2000.
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag, Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying numan genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contiguate drug and controling expression in the yeast cell with a candidate drug and controling expression in the yeast cell with a candidate drug and controling expression in the yeast cell with a candidate drug and controling expression in the yeast cell with a candidate drug and controling expression in the yeast cell with a candidate drug and controling expression in the yeast cell with a candidate drug and controling expression in the yeast cell with a method smay be used to identify candidate drugs which affect the cell cycle and for identification of anifungal drugs. AAF33268 to AAF44064 crepresent SAGE tags used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
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Matches 8; Conservative 0
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes coding sequence of a yeast gene selected from Jog previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle schemen any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate on titungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cyeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell with a candidate drug and contacting expression is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. APR33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                          Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 2 A; 1 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 2.9 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.8%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 367; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Velculescu V, Vogelstein B,
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                                                                                                                                                                                                                                                                              14-JUN-2000; 2000WO-US016223.
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                                                                                                                                                 Saccharomyces cerevisiae.
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                                                                                                         linker; PCR primer; ds.
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                                                                                                                                                                                         WO200077214-A2.
                                                                                                                                                                                                                                                                                                                        16-JUN-1999;
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AAF35204 standard; DNA; 10

AAF35204;

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising a SAGE (serial analysis of gene expression) tag. Also comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell with a candidate drug as a member of a class of drugs having contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is a ffected by the class of drugs. The NORF genes may be used to identification of phases of the cell cycle. The methods may be used to identification of antifungal drugs which affect the cell cycle and for identification of antifungal drugs. Apr3368 to AAF44064 represent SAGE tags used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                       Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method, in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 48; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                  14-JUN-2000; 2000WO-US016223
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                     23-MAR-2001 (first entry)
                                                                                                                                                                                                                            Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                        WO200077214-A2
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                               0; Gaps
30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; Live 0; Mismatches 0; Indels
                              Indels
                                 8; Conservative
                 Local Similarity
   Query Match
                   Best Loc
Matches
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RESULT 637

AAF35204/c

1 CCACCTCA 8

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CCACCTCA

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising adminstering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate continuagal drugs comprising: (a) contacting a test substance which modifies the expression of antifungal drugs comprising expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contriguous nucleotides of a NORP gene which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORP gene whose expression varies as in M1; a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and contioring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of thugs. The NORF gene may be used to identify candidate drugs which affect the cell cycle to study, monitor and affect phases of the cell cycle, the differentially captessed genes may be used as markers of phases of the cell cycle and for identification of antifungal drugs. ARF33268 to AAF33267 represent lance the resemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                              Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
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0
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                                                                                                                         Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1943.
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100.0%; Pred. No. 2.9
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Velculescu V, Vogelstein B, Kinzler K;
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                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2000; 2000WO-US016223
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                                                                                23-MAR-2001 (first entry)
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Matches 8; Conservative
                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                                                                                    linker; PCR primer; ds.
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The invention provides a method of obtaining a plant with altered content of desired protein (P1) which is regulated by cis-acting element (E1). The method involves introducing exogenous nucleic acid (ENA) construct comprising E1 which is not operably linked to coding sequence or its complement of P1, into plant cell to produce transformed plant cell, where the cell contains ENA copies to alter level of P1 in plant regenerated from cells. The method is useful for obtaining a plant, preferably transgenic tobacco plant with altered content of P1, preferably a reduced amount of infoctine, which is regulated by B1 which is a Nic gene product, where altered content of P1 may be tobacco specific nitrosamines. The present sequence represents a DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obtaining plant with altered levels of desired protein regulated cisacting element by introducing nucleic acid with the element not operably linked to coding sequence of the protein to produce a transformed cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobacco; plant; cis-acting element; transgenic; nicotine; Nic; NtQPT1; nitrosamine; beta-phaseolin; vicilin-box; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponding to the beta-phaseolin gene vicilin-box
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                                                                                                                                                                                                                                                                                                                                            Beta-phaseolin gene vicilin-box DNA sequence.
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                                                                        ABL58287 standard; DNA; 10 BP.
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                                                                                                                                                                        ABL58287;
RESULT 638
                                                  ABL58287
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New genetic variants having polymorphisms in the retinaldehyde-binding procesn I gene, useful for studying the function of and for expressing RLBP1 protein for use in screening drugs for treating diseases related to RLBP1 activity.

(GENA-) GENAISSANCE PHARM INC.

WPI; 2002-122053/16.

Choi JY, Kazemi A,

29-MAY-2001; 2001WO-US017252. 26-MAY-2000; 2000US-0207618P.

WO200192278-A2. Homo sapiens.

06-DEC-2001.

Claim 18; Page 14; 107pp; English.

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The invention relates to an isolated polynucleotide, which comprises genes and haplotypes of the retinalehyde-binding protein 1 (RLBP1) gene. The polynucleotide comprises polymorphic sites in the RLBP1 gene, which are referred to as 831-24 to designate the order in which they are located in the gene. Also included are methods for haplotyping or gene, Also included are methods for haplotyping or designate the order in which they are composition between a trait and at least one haplotype or haplotype pair of the RLBP1 gene of an individual, a method for predicting a composition between a trait and at least one haplotype or haplotype pair of the RLBP1 gene of an individual, a method for comprising a set of oligonucleotides designed to genotype or haplotype pair of the RLBP1 gene of an ear PS consisting of PS1-PS24, a kit for agencyphing the RLBP1 gene at a PS consisting of PS1-PS24, a kit for agencyphing the RLBP1 gene or individual comprising as et of oligonucleotides designed to genotype each individual comprising as the first nucleotide, where the organism expresses a RLBP1 protein encoded by the first nucleotide sequence or expresses a RLBP1 protein encoded by the first nucleotide sequence or expresses a RLBP1 contain a maino acid sequence that is a polymorphic variant sequence or expresses a RLBP1 conjumptive comprising an amino acid sequence that is a polymorphic or arier. RLBP1 protein or its fragment, and polymorphism data for the RLBP1 gene is useful in studying the comprising polymorphism and a computer system for storing and analysing comprising polymorphisms in the RLBP1 gene is useful for use organism protein or disease related to RLBP1 accession and function of RLBP1, and in expressing RLBP1 protein for expression and function of RLBP1, and in expressing RLBP1 protein for designing clinical trials of candidate drugs discovery and development process, including targeting for designing clinical trials of candidate drugs discovery and development process, including accompanies will above. The transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and testing of drugs targeted against RLBP1 protein, and for testing the efficacy of therapeutic agents and compounds for retinal diseases in a biological system. The gene for RLBP1 is located on chromosome 15q26. The present sequence is an allele specific oligomucleotide (ASO) PCR primer for amplifying a nucleic acid containing a polymorphic RLBP sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for amplifying a nucleic acid cont
using the primer extension method
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Les 8; Conservative
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0; Gaps

0; Indels Length 10;

30.8%; Score 8; DB 1; Ler 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0;

Conservative

Query Match Best Local Similarity Matches 8; Conserv

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Human, retinaldehyde-binding protein 1; ss; RLBP1; haplotype; primer; genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR; chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.

Retinaldehyde-binding protein 1 ASO primer extension primer #11.

(first entry)

09-APR-2002

ABK24238;

ABK24238 standard; DNA; 10 BP.

RESULT 639 ABK24238,

11 GCCCCTTC 18

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ABL88339,

ABL88339 standard; DNA; 10 BP.

ABL88339;

(first entry) 20-MAY-2002

Human CHRNE gene polymorphism detection primer, SEQ ID NO:73.

neuromuscular junction; skeletal muscle; postnatal development; congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; gene therapy; drug screening; primer extension; primer; ss. cholinergic receptor nicotinic epsilon polypeptide; CHRNE; chromosome 17p13-12; acetylcholine receptor; AChR

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WO200198316-A2

27-DEC-2001

20-JUN-2001; 2001WO-US019835

20-JUN-2000; 2000US-0212870P.

(GENA-) GENAISSANCE PHARM INC

Koshy B, Tanguay DA; Kliem SE, Bieglecki KM, Amaro E,

WPI; 2002-130787/17.

Novel genetic variants of cholinergic receptor, nicotinic, epsilon polypeptide gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. congential myasthenic syndrome

Claim 19; Page 15; 104pp; English.

The invention relates to a method for haplotyping the cholinergic receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an individual, and also describes 17 novel polymorphic sites within the human CHRNE gene. The CHRNE gene is located on chromosome 17pl3-12 and contains 12 exons which encode a 493 amino acid protein (ABB49112). The CHRNE protein is one of the 5 subunits of mammalian acetylcholine creceptors (AChRE) found at neuromuscular junctions in juveniles and adults, and is essential for the normal postnatal development of skeletal mysathenic syndrome (CMS). CHRNE gene are associated with congenital can function of CHRNE gene is also useful for studying the expression and function of CHRNE, and in expressing CHRNE protein for use in correnting for candidate drugs to treat diseases related to CHRNE. The method of the invention is useful for haplotyping the CHRNE gene in an individual, and can also be used in pharmaccutical research to validate candidate drugs for, treating a specific condition drugs or disease candidate drugs for, treating a specific condition drugs or disease considered to be associated with CHRNE activity such as CMS. Polymorphisms in the target region may be determined by the use of allele-specific in the target region may be determined by the use of allele-specific or candidate drugs (ABL88370-ABL88320) as probes and primers, and by primer extension using oligomucleotide primers comprising sequences ABL88371-ABL88354. The CHRNE protein is useful for improving the definition of an areliability of several steps in the discovery and drugs or discovery and drugs of an areliability of several steps; and the discovery and drugs or discover development of drugs for treating diseases associated with CHRNE activity, and may be used to screen drugs which target CHRNE. Sequences ABL083121-ABL08354 represent sequences that are specifically claimed as components of primers used to detect polymorphisms in the CHRNE gene by primer extension

ö ö a sequence which is a polymorphic variant (pV) of a reference sequence for aldo-keto reductase family 1, member BH (ARRBH) gene or its fragment, having the 22214 base pair sequence given in ABLO1105. ARRBH has antidiabetic activity and can be used in gene therapy. ARRBH can be used in the treatment of diabetes. The human ARRBH gene is located on chromosome 7q35. ABLO1107 to ABLO1129 represent allele-specific oligonucleotide (ASO) probes used in the detection of polymorphisms in the human ARRBH gene, ABLO1130 to ABLO1175 represent ASO primers used in the Ablona ARRBH gene, and ABLO1130 to ABLO1175 represent ASO primers used in the Ablona ARRBH gene, and ABLO1176 to ABLO1121 represent preferred primers used in the detection of The present invention describes an isolated polynucleotide (I) comprising Novel polymorphic variants of aldo-keto reductase family 1, member bl gene useful in studying expression and function of the protein, useful for screening drugs to treat diseases e.g. diabetes. Human; aldo-keto reductase family 1 member B1; aldose reductase; ss; AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer; allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes. Gaps Gaps ; 0 ; 0 Human AKR1B1 gene polymorphism detection primer SEQ ID NO:96. DB 1; Length 10; . 2.9e+02; ches 0; Indels Indels DB 1; Length 10; 2.9e+02; Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other; Sequence 10 BP; 2 A; 0 C; 8 G; 0 T; 0 U; 0 Other; Sanchis A; 30.8%; Score 8; DB 1 100.0%; Pred. No. 2.9 tive 0; Mismatches 30.8%; Score 8; DB 1 100.0%; Pred. No. 2.9 tive 0; Mismatches ABL01221 represent preferred primers us polymorphisms in the human AKRIBI gene Choi JY, Nandabalan K, Rounds E, Claim 18; Page 15; 103pp; English 100.0%; Pri BP. (GENA-) GENAISSANCE PHARM INC. 12-APR-2001; 2001WO-US011944. 12-APR-2000; 2000US-0196315P. ABL01199 standard; DNA; 10 12-MAR-2002 (first entry) 8; Conservative 8; Conservative CCCCTTCC 19 10 ccccrrcc 3 WPI; 2002-075056/10. Query Match Best Local Similarity Local Similarity WO200179223-A2 Homo sapiens 25-OCT-2001. 12 ABL01199; Query Match RESULT 641 Best Loc Matches Matches ABL01199, g ò 셤

RESULT 642

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ABN81474

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ABX09674;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel genetic variants of the HIV-1 Tat
interactive protein, 60 KDa (HTMIP) gene. The polymorphic variants are
useful in studying the expression and function of HTMITP, in expressing
HTMTIP protein for use in screening for candidate drugs to treat diseases
related to HTMTIP activity, in studying the effect of the variation on
the biological activity of HTMTIP and the binding affinity of candidate
drugs targeting HTMTIP for the treatment of disorders Haplotyping
methods are useful in validating HTMTIP as a candidate target for
treating a specific condition or disease predicted to be associated with
HTMTIP activity or in the dessign of clinical trials of candidate drugs
for treating a specific condition or disease associated with HTMTIP
activity. Transgenic animals are useful for studying expression of the
HTMTIP isogenes in vivo, for in vivo screening and testing of drugs
targeted against HTMTIP protein and for testing the efficacy of
that of a HTMTIP allele specific PCR primer of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                            New HIV-1 tat interactive protein, 60 kDa (HTATIP) gene polymorphic variants, for studying the expression and function of HTATIP and screening candidate drugs for treating familial glucocorticoid deficiency
                                                                                          Human; HIV-1 Tat interactive protein; HTATIP); haplotyping; genotyping;
transgenic; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     Choi JY, Gilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GITR-D mRNA SAGE tag, SEQ ID NO:158.
                                                                   Human HTATIP PCR primer SEQ ID NO 75.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Page 14; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV78447 standard; cDNA; 10 BP.
ABN81474 standard; DNA; 10 BP
                                                                                                                                                                                                                                             (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                               05-OCT-2001; 2001WO-US031593.
                                                                                                                                                                                                                      06-OCT-2000; 2000US-0238655P
                                                                                                                                                                                                                                                                     Armstrong B, Bentivegna SC,
                                            16-AUG-2002 (first entry)
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Matches 8; Conservative
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                                                                                                                                                   WO200229089-A2.
                                                                                                                              Homo sapiens
                                                                                                                                                                        11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                      screening a
                       ABN81474;
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SXCCCCCCCCCCCCXSXLLLXXBXBXBXBXBXBXXBXXBXXSXXXXXBXBX
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are expressed in activated human Thi and/or ThZ cells. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in Thi and/or Th2 cells, antibodies against these proteins, and inhibitors of the expression of groups of genes that are expressed in either or both the two cell types. Groups of genes expressed in and/or Th2 cell types and for the diagnosis and treatment of Thi and/or Th2 cell types and for the diagnosis and treatment of Thi and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human activated Th1 and Th2 cell expression gene group, useful for the diagnosis and treatment of Th1 and Th2-related diseases.
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                                         activated T cell; T lymphocyte; immune response; expression pattern; preferential expression; immune disorder; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arteriosclerosis; diagnosis; hybridisation; synergism; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
SAGE tag; serial analysis of gene expression; human; Th1 cell; activated T cell; T lymphocyte; immune response; expression pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 10; 60pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2000; 2000JP-00385816.
                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-2000; 2000JP-00385816.
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                                                                                                                                                                                                                                   JP2002186482-A.
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                                                                                                                                                            Homo sapiens
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                                                                                                                                    This invention describes a novel method for determining the genetic risk of arteriosclerosis both for clinical diagnosis and for population studies. The method comprises: (i) selecting risk-associated reference nucleic acid sequences, including their functionally characterizing mutations; (ii) applying probes from these sequences, or their complements, to a carrier; (iii) hybridising the probes with a nucleic acid from (or synthesised from) a patient sample, and (iv) detecting and evaluating the hybridisation pattern. The method provides a quick, inexpensive and informative diagnosis, and makes possible a quick, mutations or mutations that when present alone carry no risk but are risk associated in presence of other mutations. The results may be combined with known risk-assessment methods to provide a more reliable diagnosis, especially important with new therappeutic methods (e.g. gene therapy) that are directed against specific genes. All relevant mutations in a reference can be screened for in a single test and the method is constituted the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; haplotype; coagulation factor II receptor like 1; F2RL1; asthma; polymorphism; chronic pulmonary disease; inflammatory disorder; gene therapy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genetic variants having polymorphisms in the coagulation factor II
                                                                  Determining genetic risk of arteriosclerosis, for clinical diagnosis, comprises hybridizing patient nucleic acid with an array of probes derived from risk-associated reference genes and their mutations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human F2RL1 gene polymorphisms detecting primer #5.
                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                Example 1; Page 140; 146pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD44467 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanchis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                    Cullen P, Seedorf U;
                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ACCTCATC 10
                                            WPI; 2002-723374/78.
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(OGHA-) OGHAM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200255534-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD44467;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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The invention relates to an isolated polynucleotide comprising genes and haplotypes of the coagulation factor II (thrombin) receptor like 1 (FZRLI) gene bolynothic variants of the FZRLI gene are useful in studying the expression and biological function of FZRLI, and in studying the expression and biological function of FZRLI, and in coagulation associated with abnormal expression or function of FZRLI, and inflammatory disease, and inflammatory disorders. Polynucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a patient could benefit from expression or coagression of a particular FZRLI protein isoform, or an expression vector encoding the isoform may be administered to the expression vector encoding the isoform may be administered to the patient. Haplotype information is useful in improving the efficiency and cutput of several steps in drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. Information on polymorphisms may be applied in studying this protein for the treatment of disorders related to its abnormal expression or function. The invention is useful in indentifying drugs targetting expression or function. The invention is useful in a gene therapy. The
(thrombin) receptor like 1 (F2RL1) gene, useful for studying the function of F2RL1 and treating disorders associated with abnormal expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genetic variants of smoothened Drosophila homolog (SMOH) gene useful for therapeutic purposes and for expressing SMOH protein useful in identifying drugs to treat basal cell carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH; human smoothened Drosophila homologue; basal cell carcinoma; BCC; gene therapy; antisense gene therapy; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is human F2RL1 gene polymorphism detecting primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10 BP; 2 A; 1 C; 7 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                            Claim 16; Page 14; 65pp; English
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Best Local Similarity
                                                                              function of F2RL1.
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ID AAL3
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The invention relates to an isolated polynucleotide comprising a sequence which is a polymorphic variant of a reference sequence for the human consequence for a sequence for the human consequence for a sequence for a fund for argeting the polypeptide. A new method is useful for screening for darug to a sesociation between a trait such a a clinical response to a drug targeting sMOH and a haplotype of a clinical response to a drug targeting sMOH and a haplotype of targeting sMOH and a haplotype of the isolated polymorleotide is useful for studying the expression and function of SMOH and expressing considered to SMOH activity. The polymorphism and haplotype datas are useful for validating whether SMOH is a sultable target for drugs to treat BCCs, acreening for the drugs and reducing bias in clinical trials of the caruge. The isolated polymorleotide is useful for therapeutic purposes. The new method, an oligonucleotide and kit of the invention are useful for determining whether an individual has one of the haplotypes or the haplotype pairs. The polymorleotides of the invention can be used to treat disorders by gene therapy and antisense gene therapy. This smoothened brosophila homologue gene polymorphisms of the invention and sequence represents a primer used for detecting human sequence and the pagence therapy. Sequence 10 BP; 2 A; 0 C; 8 G; 0 T; 0 U; 0 Other;

Gaps ö 0; Indels 30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; ative 0; Mismatches 0; Indels Query Match Best Local Similarity 100... 8; Conservative 12 CCCCTTCC 19 CCCCTTCC 2 σ ò 셤

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ABT14399 standard; DNA; 10 BP. 20-FEB-2003 ABT14399; RESULT 647 ABT14399,

(first entry)

Nucleic acid PCR amplification method-related RAPD PCR primer #169.

Nucleic acid amplification; nucleic acid analysis; BNA analysis; RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

Unidentified

40200281743-A2

28-MAR-2002; 2002WO-GB001489

32-APR-2001; 2001GB-00008182

(HAMI/) HAMILL B.

Hamill

WPI; 2003-075484/07.

Amplification of nucleotide sequences from polynucleotides by chain extension of oligonucleotide primers, comprises 2 oligonucleotides in solution, 2 attached to supports and both share complementary sequences.

Disclosure; Fig 17; 60pp; English.

The invention comprises a method for the PCR amplification of nucleic acids. The method involves a set of primers, where two of the primers are in solution and at least two other primers are attached to a solid support. The method of the invention can be used for the analysis of a

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RESULT 64 ADH56997

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nucleic acid or a mixture of nucleic acids, including: single-stranded DNA molecules, double-stranded DNA molecules and mRNA molecules. The present DNA sequence represents a random amplified polymorphic DNA (RAPD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amplification of nucleotide sequences from polynucleotides by chain extension of oligonucleotide primers, comprises 2 oligonucleotides in solution, 2 attached to supports and both share complementary sequences.
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                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid PCR amplification method-related RAPD PCR primer #144.
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                                                                                                         30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02;
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                                                                          Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
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                                                                                                                   100.0%; Pred. ....
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                                             PCR primer of the invention
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                                                                                                                        Local Similarity 100.
nes 8; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel single nucleotide polymorphisms within the human CARD4 gene. Specifically, it refers to allelic variants of CARD4 (NOD1), a member of the CED4/Apaf-1 family that is involved in caspase-9 induced apoptosis and inflammation. The present invention describes a kit for determining the allelic variants of CARD4 polymorphic regions of an individual, which can be useful for predicting susceptibility, as well as diagnosis, prevention and treatment of various disorders including chronic obstructive pulmonary disease, rheumatoid
                                                                                                  ss; human; CARD4; NOD1; CED4/Apaf-1; caspase-9 induced apoptosis;
inflammation; Afronic obstructive pulmonary disease;
rheumatoid arthritis; inflammatory bowel; psoriasis; asthma;
antiasthmatic; antiinflammatory; antiallergic; pharmacogenomic; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis, inflammatory bowel disease, psoriasis or asthma. Accordingly, the compositions of this invention exhibit antiasthmatic, antiinflammatory and antiallergic activities. Furthermore, they may be used to identify patients that would be strong candidates for effective treatment with a CARD4 modulator, in pharmacogenomics, or in monitoring the effects of CARD4 therapeutics during clinical trials. The nucleic acid molecule may also be used in forensics or paternity testing. This oligonucleotide sequence is a human CARD4 DNA oligo that indicates an intron/exon boundary of the genomic CARD4 DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid molecule comprising an allelic variant of a CARD4 gene, useful for diagnosing, preventing or treating asthma or an apoptotic, inflammatory or allergic disorder, or in pharmacogenomics.
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0
                                                                          Human CARD4 5' intron DNA oligo preceding exon 8 SeqID 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.9e+02; Live 0; Mismatches 0; Indels
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ADH56997 standard; DNA; 10 BP.
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ID ADK12942 standard; DNA; 10 BP.
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                                                 (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                            (BARN/) BARNES G.
(BERT/) BERTIN J.
                                                                                                                                                        paternity testing
                                                                                                                                                                                                         US2003219810-A1.
                                                                                                                                                                                 Homo sapiens.
                                                 25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                 Barnes G,
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                         ADH56997;
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20-MAY-2004 (first entry)

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The present invention describes a method (M1) for aiding in the diagnosis of glioma. (M1) involves detecting an expression product of at least one gene (I) in a first brain tissue sample (T) suspected of being neoplastic, where (I) is chosen from any one of 255 genes (glioma comparation, where (I) is chosen from any one of 255 genes (glioma comparation, where (I) in (T) with expression of (I) in a second normal brain tissue sample (R), where increased expression of (I) in a second normal brain tissue sample (R), where increased expression of (I) in a second normal brain tissue sample (R), as likely to be neoplastic. Also described: (1) creating (M2) glioma involves contacting cells of the glioma with an antibody that specifically binds to a extracellular epitope; (2) dentifying (M3) a test compound with the cell which expresses contacting a test compound with the cell which expresses the at least one gene and dentifying test compound as a potential anticancer drug if it decreases the expression of at least one gene; (3) identifying (M4) a test compound cy at age as described above, monitoring mRNA of the gene, and cidentified by a tag as described above, monitoring mRNA of the gene, and identifying the test compound as a potential anticancer drug if it compound with the cell which expresses mRNA of at least one gene inducting (M5) an immune response to glioma involves administering to a mammal, a protein correction of glioma cells, and as immune response inducers. (M1) is useful for aiding in diagnosing glioma. (M2) is useful for treating multicarrance and plane and mammal who has had a glioma surgically removed. The present sequence represents a human GN response to a glioma in a human. (M3) is useful to mammal a human general invariation of the expansion of the present sequence represents a human of the present invariation of the present in a mammal human of the present invariation of the present invarious or in a mammal succession of the present invarious in the exemplification of the present invarious or in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing glioma by detecting expression product of any one of 255 genes, glioma endothelial markers, in brain tissue sample suspected of being neoplastic, and comparing the expression with expression in normal brain tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                           glioma; brain tissue; neoplastic; glioma endothelial marker; GEM; anticancer; antiglioma; immune response; cytostatic; multi-drug sensitive glioma; human; standard tag; ss.
Human glioma endothelial marker (GEM) standard tag SEQ ID NO:120.
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100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-2003; 2003WO-US025614.
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01-APR-2003; 2003US-0458978P.
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 TCCTAAGC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004016758-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Madden SI,
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(ISIS-) ISIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ7363
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                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a method of screening for candidate agents capable of altering the biological activity of a protein encoded by a nucleotide involved in hypoxia-related tumourigenesis. The method of the invention involves: contacting a test agent with a target cell expressing the nucleotide, and monitoring the activity of the expressed protein product; if the test agent modifies the activity of the expressed protein then this is a candidate agent. The method of the invention is useful for modifying hypoxia-induced gene regulation and for diagnosing, prognosing or treating tumours. The present DNA sequence represents a SAGE tag that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                            Identifying agents that alter biological activity of a polypeptide encoded by a polypuclectide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity of expressed product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of oligonucleotide set D1 for binding to the HIV gag-pol triple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide, target molecule, binding activity, therapy, HIV, diagnosis, research, gag-pol; triple strand, ss.
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                                                                                    Hypoxia-related tumourigenesis-related SAGE tag #1795.
                                                                                                         screening; hypoxia-related tumourigenesis;
hypoxia-induced gene regulation; tumour; SAGE tag; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 3 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 92; 100pp; English.
                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ37873 standard; RNA; 11 BP.
                                                                                                                                                                                                     09-APR-2004; 2004WO-US011087.
                                                                                                                                                                                                                          09-APR-2003; 2003US-0461712P.
                         ADUZ0004 standard; DNA; 10
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                                                                                                                                                                                                                                               (GENZ ) GENZYME CORP
                                                                                                                                                                                                                                                                                       WPI; 2004-758333/74.
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                                                                                                                                                            WO2004092198-A2.
                                                                 13-JAN-2005
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04-JUL-1993
                                            ADU20004;
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                                                                                                                                                                                                                                                                   Nacht M;
     RESULT 651
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The example concerns random oligo set binding to HIV gag-pol triple strand. Binding to double stranded DNA or RNA is possible by formation of a three stranded complex with the incoming third strand binding to the major groove of the duplex RNA or DNA. To determine the best oligo to bind to the gag-pol stem loop, a group of RNA oligo sets was designed to bind to the purine-rich strand of the gag-pol stem-loop. At the posn. of the two Cys the sequence was randomised to provide the sequences in AAQ37870- AAQ37877. Binding to the gag-pol stem-loop was measured by gel shift analysis. In round 1, oligo set Cl had the greatest affinity, in the second round C was fixed in the eighth posn. and the ninth posn. was determined. Oligo set C2 had the greatest affinity for the target in the ninth round. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening of oligo:nucleotide and polypeptide molecules - by synthesising sets of molecules and assaying for activity against a target molecule.
                                                                                                                                                                                                                                                                                                                                                       Vickers T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA oligonucleotide with binding affinity for HIV gag-pol stem loop.
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                                                                                                                                                                                                                                                                                                                                                       Hanecak RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.8%; Score 8; DB 1; 62.5%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                       Anderson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Wyatt J, Bruice TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 38; 75pp; English
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                                                                                                                                                                       92WO-US007121.
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(first entry)
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                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-094029/11.
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Best Local Similarity
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                                                   WO9304204-A1
                                                                                                                                                                       21-AUG-1992;
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13-JUN-1995
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                                                                                                             04-MAR-1993
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Synthetic.
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Davis P;
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                                                                                                                                                  (I) which modulate transcription factor function for therapeutic, diagnostic or research purposes. Binding of (I) to double stranded DNA or RNA is possible by formation of a three stranded complex with the incoming third strand binding in the major groove of the duplex RNA or DNA. One of the limitations in the design of triple strand interactions is the need to have a long stretch of homopurines as a target. The 3' (right) side of the gag-pol stem loop is homopurine except for a pair of cytosines near the bottom of the stem loop is homopurine except for a pair of their affinity for the stem loop was measured in a gel shift assay. AAQT3631 had the greatest affinity for the target with a Kd of 50 in round 1. In round 9, AAQT3635 had the greatest affinity for the target with a Kd of 1. This showed that a triple strand binding sequence can be optimised. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligonucleotide synthesis; unrandomisation; HIV gag-pol; HIV TAR element; ss.
                                                        Identifying oligo-nucleotide(s) binding specifically to transcription factors - or other target molecules, using sets of oligo-nucleotide(s) with a fixed base at some positions and randomised bases at other, and interaction with selected set.
                                                                                                                                        method of the invention is useful for identifying oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wyatt J, Anderson K, Ecker DJ, Vickers T, Hanecak R, Freier SM;
Sanghvi YS, Brown-Driver V, Cook PD, Davis P, Bruice TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Random oligonucleotide set D1 binding to HIV gag-pol triple strand.
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                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                               30.8%; Score 8; DB 1; Length 11; 62.5%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                        Sequence 11 BP; 0 A; 6 C; 0 G; 0 T; 4 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                  Example 23; Page 44; 106pp; English.
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            Davis PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV06737 standard; RNA; 11 BP.
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94US-00196103
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(first entry)
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Matches 5; Conservative
           Ecker DJ, Vickers TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                              13 CCCTTCCT 20
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                                  WPI; 1994-317042/39
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triple strand;
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22-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                               Query Match
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This sequence represents an oligonucleotide set shown in the specification. The invention relates to a method for determining an oligonucleotide having an assayable activity for a target molecule. It comprises: (a) preparing a group of sets of oligonucleotides of substantially the same length, each oligonucleotide comprising at least 3 nucleotides by defining a common position in the oligonucleotides of the sets, and synthesising the sets of oligonucleotides so that each set has a different nucleotide in the common position, the nucleotides which are not in the common position, sets (b) assaying each of the not in the common position and lecting the set of having the highest activity against the target molecule; (c) selecting the set of coligonucleotides of the substantially same length, each of the sets of the further group having in the previoually defined common position the nucleotide appearing in that position in the set selected in step (c), and having in an additional defined common position a different nucleotide, the nucleotides in the positions of the oligonucleotides ö which are not in a defined common position being randomised; (e) assaying each of the sets of the further group for the assayable activity; (f) selecting the set of the further group having the highest assayable activity; and (g) repeating steps (d) to (f) until an oligonucleotide having the assayable activity for the target molecule is determined. The methods can be applied to any molecules that can be oligomerised in a controlled fashion. (Updated on 25-MAR-2003 to correct PF field.) Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial Gaps Human; skin ageing; skin stress; EST; expressed sequence tag; ss. .; 0 0; Indels DB 1; Length 11; 3e+02; Human skin stress/ageing related EST SEQ ID NO 998. Sequence 11 BP; 0 A; 6 C; 0 G; 0 T; 4 U; 1 Other; (Updated on 25-MAR-2003 to correct PI field.) 3; Mismatches 30.8%; Score 8; 62.5%; Pred. No. Hofmann Claim 8; Page 78; 325pp; German. ABQ87243 standard; cDNA; 11 BP. 20-DEC-2001; 2001WO-EP015178. 03-JAN-2001; 2001DE-01000121 (first entry) Σ 5; Conservative Conradt CCCTTCCT 20 1 cccouccu 8 (HENK) HENKEL KGAA. WPI; 2002-528865/56. Local Similarity WO200253773-A2. Homo sapiens. Petersohn D, 10-SEP-2002 11-JUL-2002. expression. AB087243; 13 Query Match RESULT 655 ABQ87243/c Matches

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analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential sychisms. (A) comprises protein or mRNAMs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of sharmacutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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0
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                                                                                                                                                                                                                                         30.8%; Score 8; DB 1; Length 11;
100.0%; Pred. No. 3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human skin stress/ageing related EST SEQ ID NO 1338.
                                                                                                                                                                                                    Sequence 11 BP; 2 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ87583 standard; cDNA; 11 BP.
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                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                        17 TCCTAAGC 24
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                                                                                                                                                                                                                                                           Local Similarity
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acnes; sebororrhes; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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100.0%; Pred. No. 3e+
:ive 0; Mismatches
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Query Match 30.8%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 8; Conservative 0; Mismatches 0; Indels

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ABV71517;
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                   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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100.0%; Pred. No. 3e+
ive 0; Mismatches
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disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cill carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Sequence 11 BP; 1 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; sclaroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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  Claim 24; Page 299; 1345pp; German.
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(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriacis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; cosecea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                      In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
                                                                                                           Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGB, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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100.0%; Pred. No. 3e+02;
Live 0; Mismatches (
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                      BP.
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                     ABV68306 standard; cDNA; 11
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                                                                                      Human skin EST 6092.
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                                                                                                                                                         Homo sapiens
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RESULT 663
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Matches
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (GM1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis, acne; seborrhea; lupus expressedsus inchancial call carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                                                                                                                                                                                                                                                                                                                     Hofmann K;
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                                            In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                          Disclosure; Page 110; 1345pp; German.
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  Hofmann K;
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Best Local Similarity 100.00
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                                                                       e.g. skin cancer.
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 Petersohn D,
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                         (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
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(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                    In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                             Hofmann K;
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                                                                                                            ABV65863 standard; cDNA; 11 BP.
 100.08;
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Query Match
Best Local Similarity 100.
Matches 8; Conservative
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            8; Conservative
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 Similarity
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                                                                                                                                                                                                                                            Homo sapiens.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                  Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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100.0%; Pred. No. 3e+
tive 0; Mismatches
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Human skin EST 573
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The invention relates to in vitro identification (M1) of genes expressed en the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn, psoriasis, seleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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pain transmission; primary sensory neuron; transcription factor;
detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;
                                                                                                                                                                                                    In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                      Hofmann K;
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                                 20-DEC-2001; 2001WO-EP015179.
                                                                    03-JAN-2001; 2001DE-01000127
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                     Petersohn D,
 11-JUL-2002.
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This invention describes a novel nucleic acid containing a specific segment having at least one region that modulates expression of the VRI (vaniloid receptor type 1) receptor; or a functional derivative, allele or fragment of this region, or a sequence that hybridises to it under standard conditions. The VRI modulator is derived from one or more of positions 221315-22314 of GenBank AL670399, 31673-3559 of AL663116, or 44731-4231 or 36616-3315 of AR168787 and is involved in transmission of pain, particularly in primary sensory neurons. The invention also ce describes a vector that contains the VRI modulator, host cells containing this vector (other than human germ or embryonal stem cells) and a method for modulating expression of the VRI receptor by introducing the conducts of the vector into a cell that contains the VRI gene. The products of the invention are used for detecting a transcription factor from its binding to a regulatory sequence (or a double-stranded colligonucleotide fragment of it), e.g. by Western blotting or enzymetriance with overexpression or underexpression of the transcription associated with overexpression or underexpression of the transcription factor. The region that modulates VRI receptor expression includes a chinding site for a transcription factor, e.g. MZFI, NFkappaB, NFAT or GATAI. The nucleic acids of the invention, or vectors containing them, census and myalgia, that are associated with activity of the VRI exemptor in a remarking a factor. This sequence represents a fragment of murine VRI exon 1d DNA centering in a case of the presents a fragment of murine VRI exon 1d DNA centering the containing them. New nucleic acid that modulates expression of the vanilloid receptor-1, useful for control of pain or sensitivity disorders, comprises sequences Gaps hair-bearing skin; human; serial analysis of gene expression; SAGE; homeostasis; cosmetic; pharmaceutical; biochip; ds. ö Human hair-bearing skin-associated DNA fragment SEQ ID NO 1090. Holtkoetter O; 30.8%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels which is capable of binding to a transcription factor. Sequence 11 BP; 3 A; 6 C; 0 G; 2 T; 0 U; 0 Other; Gassenmeier T, from control regions of the receptor gene. Disclosure; Page 50; 68pp; German. ADQ36273 standard; DNA; 11 BP. 30.8%; 20-DEC-2002; 2002DE-01060931 20-DEC-2002; 2002DE-01060931 , Schlotmann K, Hofmann K; (first entry) Query Match Best Local Similarity 100. CACCTCAT 11 σ (HENK) HENKEL KGAA. WPI; 2004-518857/50. DE10260931-A1 Homo sapiens 23-SEP-2004 Petersohn D, 08-JUL-2004. Conradt M, ADQ36273; ~ RESULT 672 ADQ36273 ð 셤 ö Gaps

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This invention describes a novel in vitro method for identifying genes that are significant for hair-bearing skin in humans. The method comprises recovering from hair-bearing skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixtures from skin on which hair does not grow and subjecting both mixtures to serial analysis of gene expression (SAGS) to identify those genes for which expression is markedly different between the two types of skin. The invention also describes in vitro methods for determining homeostasis of human hair-bearing skin and for determining activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human hair-bearing skin. A biochip and a test kit comprising a solid support (lexible or rigid) with immobilised probes are also described for determining homeostasis. The hair-bearing skin is from the scalp and the other skin is from the face. The method allows identification of as many as possible of the genes important for hair-bearing skin, and therefore, of a very wide range of potential therapeutic and cosmetic agents. AD035184-AD036518 represent harming whin a hair-bearing with hair-bearing with hair-bearing with hair-bearing with a dentify genes associated with hair-
In vitro identification of genes important for hair-bearing skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
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                                                                                                                           Claim 4; SEQ ID NO 1090; 250pp; German
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            100.0%; Pred. No. 3e+02;
iive 0; Mismatches 0; Indels
30.8%; Score 8; DB 1; Length 11;
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            Local Similarity
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ADQ35036 standard; DNA; 11 BP.
             (first entry)
             23-SEP-2004
         ADQ35036;
RESULT 673
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Human facial skin-associated DNA fragment SEQ ID NO 3126.

facial skin; human; serial analysis of gene expression; SAGE; homeostasis; biochip; cosmetic; pharmaceutical; ds.

DE10260928-A1 Homo sapiens

08-JUL-2004

20-DEC-2002; 2002DE-01060928.

20-DEC-2002; 2002DE-01060928

HENK) HENKEL KGAA.

Holtkoetter O; Gassenmeier T, Petersohn D, Schlotmann K, Conradt M, Hofmann K; Conradt M,

WPI; 2004-518855/50.

In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.

Claim 4; SEQ ID NO 3126; 577pp; German.

This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises recovering, from facial skin in humans. The method comprises (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to sarial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin; a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or the december of the control of the cont ö disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention. This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises recovering, from facial skin, a first mixture of genetically expressed In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis. Gaps ; facial skin; human; serial analysis of gene expression; SAGE; homeostasis; biochip; cosmetic; pharmaceutical; ds. ö 30.8%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 3e+02; cive 0; Mismatches 0; Indels Gassenmeier T, Holtkoetter Human facial skin-associated DNA fragment SEQ ID NO 462. Seguence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other; Claim 6; SEQ ID NO 462; 577pp; German. BP. 20-DEC-2002; 2002DE-01060928. 20-DEC-2002; 2002DE-01060928 Schlotmann K, ADQ32372 standard; DNA; 11 (first entry) 8; Conservative Petersohn D, Schloumen S; 14 CCTTCCTA 21 σ (HENK) HENKEL KGAA. WPI; 2004-518855/50. Query Match Best Local Similarity CCTTCCTA DE10260928-A1. 23-SEP-2004 Homo sapiens. 08-JUL-2004. ADQ32372; RESULT 674 Matches g ઠે

(SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin, a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic agents. ADG13111 represent human DNA Tag fragments used to

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identify the facial skin-associated genes described in the invention.

Sequence 11 BP; 2 A; 2 C; 7 G; 0 T; 0 U; 0 Other;

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  (transcribed and optionally translated) factors (i.e. proteins, mRNA or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ34254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 675
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Gaps .; 0

ö In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis. Gaps ; 0 facial skin; human; serial analysis of gene expression; SAGE; homeostasis; biochip; cosmetic; pharmaceutical; ds. Gassenmeier T, Holtkoetter O; 0; Indels Length 11; Human facial skin-associated DNA fragment SEQ ID NO 510. 30.8%; Score 8; DB 1; L 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0 Claim 6; SEQ ID NO 510; 577pp; German. ADQ32420 standard; DNA; 11 BP. 20-DEC-2002; 2002DE-01060928. 20-DEC-2002; 2002DE-01060928 Schlotmann K, (first entry) 8; Conservative Conradt M, Hofmann K; Query Match Best Local Similarity CGCCCCTT 17 (HENK) HENKEL KGAA. CGCCCCTT 1 WPI; 2004-518855/50. DE10260928-A1. Homo sapiens Petersohn D, 23-SEP-2004 08-JUL-2004. ADQ32420; 10 RESULT 676 Matches ADQ32420 셤 8 X X X H

This invention describes a novel in vitro method for identifying genes recovering, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin; a test kit which comprises a solid support (flexible or rigid) on which are

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This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises recovering, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression

In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.

WPI; 2004-518855/50.

Claim 4; SEQ ID NO 2344; 577pp; German.

Page 302

immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention.

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Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Gaps ; 0 Similarity 100.0%; Pred. No. 3e+02; 8; Conservative 0; Mismatches 0; Indels DB 1; Length 11; 13 CCCTTCCT 20 3 cccrrccr 10 Query Match Best Local Similarity Matches g ઠે

RESULT 677 ADQ35105,

Human facial skin-associated DNA fragment SEQ ID NO 3195. ADQ35105 standard; DNA; 11 BP. (first entry) facial skin; homeostasis; 23-SEP-2004 ADQ35105;

human; serial analysis of gene expression; SAGE; biochip; cosmetic; pharmaceutical; ds.

DE10260928-A1

08-JUL-2004

20-DEC-2002; 2002DE-01060928.

20-DEC-2002; 2002DE-01060928

(HENK) HENKEL KGAA

Holtkoetter O; Gassenmeier T, Schlotmann K, Hofmann K; Petersohn D, Conradt M,

In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.

WPI; 2004-518855/50

Claim 4; SEQ ID NO 2626; 577pp; German.

WPI; 2004-518855/50.

for In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.

Claim 3; SEQ ID NO 3195; 577pp; German.

This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises recovering, from facial skin in humans. The method comprises (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes and in vitro method for determining homeostasis of human facial skin, a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin, are immobilised probes that bind specifically to the factors of interest and a biochip for odetermining homeostasis of human facial skin, the products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or

This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises crecovering, from facial skin, a first mixture of genetically expressed transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an vitro method for determining homeostasis of human facial skin; a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin; The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic

ö identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to disturbances of the homeostasis of human skin and a screening method for identify the facial skin-associated genes described in the invention. Gaps ; 0 facial skin; human; serial analysis of gene expression; SAGE; homeostasis; biochip; cosmetic; pharmaceutical; ds. Holtkoetter O; Human facial skin-associated DNA fragment SEQ ID NO 2626. 30.8%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other; Gassenmeier T, BP. 20-DEC-2002; 2002DE-01060928. 20-DEC-2002; 2002DE-01060928 Schlotmann K, ADQ34536 standard; DNA; 11 (first entry) 8; Conservative Hofmann K; N (HENK) HENKEL KGAA. 2 CACCICAL 9 Query Match Best Local Similarity CACCTCAT DE10260928-A1. Petersohn D, Homo sapiens 23-SEP-2004 08-JUL-2004. Conradt M, ADQ34536; agents RESULT 678 Matches ADQ3453(

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WPI; 1993-386599/48.
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agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention.
                                                                                                                                                                                          RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA; picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV; papilloma virus; HPV; Estain-Barr virus; BBV; TCIV; T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus; influenza virus; HSV; herpes simplex virus; vector; immune response; antibody; ribozyme; viral RNA; treatment; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dudycz LW, Mcswiggen JA, Macejak DG, Holecek JJ;
                                     30.8%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                      Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                            Herpes simplex virus target sequence 104.
                                                                                                                                                                                                                                                                                                           92US-00882689.
92US-00882713.
92US-00882713.
92US-00882813.
92US-0088288.
92US-00882889.
92US-00882889.
92US-00882889.
92US-00882889.
92US-00882819.
92US-00882813.
92US-00884473.
92US-00884431.
92US-00884423.
92US-00884423.
92US-00884423.
92US-00884423.
92US-00884423.
92US-00884423.
92US-00884423.
92US-0098483.920.
92US-00986859.
                                                                                                                       AAQ53026 standard; RNA; 11 BP.
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                                                                                                                                                              (first entry)
                                                     8; Conservative
                                                                                                                                                      (revised)
                                                                             CTTCCTAA 10
                                                                   CTTCCTAA 22
                                             Local Similarity
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14-MAY-1992;
14-MAY-1992;
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26-MAY-1994
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14-MAY-1992;
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14-MAY-1992;
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14-MAY-1992;
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Mamone JA;
                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                      AAQ53026;
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                                      Query Match
                                                                                                        RESULT 679
                                              Best Loc
Matches
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                                                                                                                                          The sequences (AAQ52923-Q53037) are pref. herpes simplex virus target sequences for enzymatic RNA molecules. The RNA molecules are complementary to a substrate binding region in the specified gene target. They also have enzymatic activity, in that they specifically cleave RNA in the target. The ERMs interfere with viral replication and therefore have anti-viral properties. They can be used to attenuate viruses to be used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel non-MRL healer mouse (M) having at least one quantitative trait locus selected from those given in the specification, exhibiting an enhanced healing response to a wound compared to mice (m) without the locus. The invention describes a novel method of identifying a gene involved in enhanced wound healing by identifying DNA microsatellite markers which can distinguish healer mice from non-healer mice and identifying microsatellite markers which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian model for enhanced wound healing - useful for identifying
Enzymatic RNA molecules - used to inhibit viral replication, infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wound healing, non-MRL healer mouse, quantitative trait locus; QTL; healing response; microsatellite marker; treatment; central nerve; peripheral nerve; nerve injury; SAGE tag; murine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.0%; Score 7.8; DB 1; Length 11; 63.6%; Pred. No. 3.2e+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 BP; 0 A; 8 C; 1 G; 0 T; 2 U; 0 Other;
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                                                                                           Claim 5; Fig 15; 287pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ18930 standard; DNA; 11 BP.
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98US-0097937P.
98US-0102051P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999 (first entry)
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                                  gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                field.)
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segregate with enhanced wound healing in progeny of the mice, where a chromosomal locus containing at least one enhanced wound healing gene is identified. A method of treating a wound in a mammal is also disclosed. The new methods are useful for treating wounds, especially central and peripheral nerve wound. The methods of the invention are useful for restoring function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes and gene products involved in enhanced wound healing, and to provide methods for wound healing. AA218691-219036 represent murine SAGE tags from C57BL/6 and MRL mice which are used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                     nvention
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G; 5 T; 0 U; 0 Other; Sequence 11 BP; 2 A; 1 C; 3

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Gaps
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30.0%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 3.2e+02; ive 0; Mismatches 2; Indels
                             9; Conservative
                                                       15 CTTCCTAAGCA 25
                                                                          11 CATCATAAGCA 1
               Local Similarity
  Query Match
                             Matches
                 Best
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Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds.
                                          Triple helix forming nucleotides 1153-1163 of the p53 gene.
           AAX14968 standard; DNA; 11 BP.
                                                                                                                   92US-00968436.
                                                                                                        93US-00173489
                                (first entry)
                                24-MAR-1999
                                                                       Homo sapiens
                                                                                                        22-DEC-1993;
                                                                                                                    29-OCT-1992;
                                                                                 US5861244-A.
                                                                                             19-JAN-1999
                     AAX14968;
RESULT 681
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(PROF-) PROFILE DIAGNOSTIC SCI INC. Wang C; Hepburn AG,

WPI; 1999-130384/11.

Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria.

Disclosure, Col 25-26; 168pp; English.

This sequence represents a transcription factor binding site identified in the human P15B3 promoter. The invention relates to sequences AAA87725-88774 which encode human secreted proteins AAB2563-B25812. The proteins include signal peptides. The P15B3 promoter is used in the isolation of the CDNAs of the invention. Included in the invention are a host cell containing one of the CDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the CDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted brotsein. The CDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention

immunological

may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunologica, disorders, anyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease,

dementia, hyperlipidaemia, septic shock and impotence Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping procedures.

Example 48; Fig 5; 306pp; English.

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WPI; 2000-442637/38. Bougueleret L,

The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-erranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (DNy detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus

Sequence 11 BP; 0 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

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                                                                                                                                                                                   Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autofimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atheroselerosis; Alzheimer's disease; neurodegenerative disorder; rejection; dementia; hyperlipidaemia; septic shock; impotence; promoter; P1583; ds.
                            Gaps
                            ;
0
                                                                                                                                                                  Promoter P15B3 transcription factor binding site SEQ ID #159.
         Score 7.8; DB 1; Length 11;
Pred. No. 3.2e+02;
); Mismatches 2; Indels
                           0; Mismatches
                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                  99WO-IB002058
                                                                                                                                                                                                                                                                                                                                   98US-0113686P.
                                                                                                                                                                                                                                                                                                                                            99US-0141032P.
          30.0%;
81.8%;
Query Match
Best Local Similarity 81.55,
Thes 9; Conservative
                                                                                                              AAA87795 standard; DNA; 11
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                                                                 1 CTCCTCTCCCC 11
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                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                 28-NOV-2000
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                                                                                           RESULT 682
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(first entry)

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Human; expressed sequence tag; EST; ds; promoter P15B4; acute myocardial infarction; acute ischaemic stroke; diabetes; anaemia; growth hormone deficiency; hepatitis; kidney carcinom; multiple sclerosis; chemotherapy-induced neutropaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified 5' expressed sequence tags useful in diagnostic, forensic, gene therapy or chromosome mapping procedures, or for distinguishing human tissues or cells from non-human tissues or cells.
                                                                             Human transcription factor binding site from promoter P15B4 #5.
                                                                                                                                                                                         transcription factor binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 53; Fig 5; 90pp; English.
                                                                                                                                                                                                                                                                                                                                    27-JUL-2000; 2000EP-00202699.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-357986/38.
                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                        05-AUG-1999;
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                                         23-OCT-2001
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     AAS07926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for selecting PCR primers for nucleic acid amplification. The method comprises determining the melting temperature (T_m) range for degenerate olisyouncleotide primers with a fixed sequence portion (FS) and a degenerate-sequence portion (DS) by searching known portion of a nucleic acid template for a sequence complementary to a desired FS of a primer. Nucleotide base pairs flanking or interspersed between the sequence complementary to a DS of one of the primers are detected and T_m is calculated. The method of the present invention allows primers which produce more efficient DNA amplification to be produced. The present sequence is a primer. This sequence was used to exemplify the occurence of a primer with a FS of 6 base pairs (CGGCCC) within a template. The remaining 5 base pairs make up the DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining Tm range for several degenerate primers with a fixed-sequence and a degenerate-sequence portion for use in polymerase chain reaction amplification by identifying a specific sequence in the nucleic acid
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                             PCR primer; nucleic acid amplification; melting temperature; T_m; ss.
                                                        ;
                      Length 11;
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                                                                                                                                                                                                                                                                                                                           Oligonucleotide #4 used in a method for primer selection.
                                                      2; Indels
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                  Score 7.8; DB 1;
Pred. No. 3.2e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                   AAC63231 standard; DNA; 11 BP.
                30.0%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-US008962.
                                                                                                                                                                                                                                                                                         06-FEB-2001 (first entry)
Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                    9 TCGCCCCTTCC 19
                                                                                                                     TCCCACCTTCC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Senapathy P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      template
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Jobert S, Giordano J;

99US-0147499P

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The sequence represents a transcription factor binding site from human promoter P1584, the promoter and binding site being isolated using promoter P1584, the promoter and binding site being isolated using correct from one of the 5' expressed sequences tags (EST) of the invention, one of 15442 nucleotide sequences not given in the specification. The 5' EST may be used to efficiently identify and isolate CC subtranlated regions (UTRS) and upstream regulatory regions which control the location, developmental stage, rate and quantity of protein synthesis, as well as the stability of the mRNA. ESTS containing the 5' ends of protein genes may include sequences for chromosome mapping and identification individuals. The EST may further be used to distinguish human tissues or cells from non-human tissues or cells that do not and do not express conformation include full protein coding sequences, to obtain and express conformation include full protein coding sequences of the corresponding gene products, to map and clone promoter regions, and open reading frames from a genomic sequence, and to obtain and express corresponding pene products, to map and clone promoter regions, and open reading portions of the protein. EST-related nucleic acids are useful in forensic procedures or in diagnosis of genetic comparation map of human chromosomes, and in gene therapy to control or treating or controlling a variety of human conditions e.g acute controlling a variety of human conditions e.g acute myocardial infarction, acute ischaemic stroke, diabetes, anaemia, growth chromoe deficiency, hepatilish, kidney carcinoma, multiple sclerosis, chemotherapy-induced neutropaenia
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RESULT 685 ABV65218

AAS07926 standard; DNA; 11 BP.

RESULT 684 AAS07926

10 CGCCCCTTCCT 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                    Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 108; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hofmann K;
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BP.
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ABV65218 standard; cDNA; 11
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                                                                                   (first entry)
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                                                                                                                              Human skin EST 3004
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les 9; Conserv
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                                        ABV65218;
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Matches
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(M1) is useful for identifying genes and quantify their expression.

(M2) is useful for identifying genes involved in skin homeostasis; to be determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atoppic dermatitis; acne; sebornhea; lupus expressedsus rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                20-DEC-2001; 2001WO-EP015179.
                                                                                                                                                                                                     03-JAN-2001; 2001DE-01000127
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. skin cancer.
WO200253774-A2
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WPI; 2002-590638/63

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin discretes, specifically neurodermatitis; sumburn; psoriasis; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
                                                                                                                                                                                                                             Disclosure; Page 178; 1345pp; German.
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30.0%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 3.2e+02; tive 0; Mismatches 2; Indels
Sequence 11 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
            Query Match
Best Local Similarity 81.0
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
              ABV68399 standard; cDNA; 11 BP.
                                                                                                                                                       20-DEC-2001; 2001WO-EP015179
                                                                                                                                                                      03-JAN-2001; 2001DE-01000127
                                             (first entry)
                                                           Human skin EST 6185
                                                                                                                       WO200253774-A2
                                            21-OCT-2002
                                                                                                          Homo sapiens
                                                                                                                                       11-JUL-2002
                             ABV68399;
RESULT
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(HENK ) HENKEL KGAA
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Disclosure; Page 196; 1345pp; German. e.g. skin cancer.

Hofmann

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Conradt

Petersohn D,

WPI; 2002-590638/63

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to

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              promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                          Gaps
     or
 determine skin homeostasis and to test agent (A) that maintains
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                                                                                                                                                                      Score 7.8; DB 1; Length 11;
Pred. No. 3.2e+02;
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                                                                                                                                    Sequence 11 BP; 0 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
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9; Conservative
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                                                                                                                                                                                                                                                                   CGCCGCTTCTT
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss. Human skin EST 7692

BP.

ABV69906 standard; cDNA; 11

ABV69906 ID ABV6

(first entry)

21-OCT-2002

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Gaps ö

ABV69906;

20-DEC-2001; 2001WO-EP015179 WO200253774-A2 Homo sapiens. 11-JUL-2002

Hofmann K; 03-JAN-2001; 2001DE-01000127 Σ̈́ Conradt WPI; 2002-590638/63. (HENK) HENKEL KGAA. Petersohn D,

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Claim 24; Page 245; 1345pp; German. e.g. skin cancer.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (\$AGE\$) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sumburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacca, melanoma, basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag of the invention

Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Gaps ö Score 7.8; DB 1; Length 11; Pred. No. 3.2e+02; 0; Mismatches 2; Indels 30.0%; 81.8%; 9; Conservative Query Match Best Local Similarity Matches 9; Conserv

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RESULT 692
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; sosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                      Human; skin, dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                          Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Human skin EST 7414
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Best Local Similarity
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; scleroderma;
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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                                                                                                   Hofmann K;
                                                                                                                                                                                                                             Disclosure; Page 33; 1345pp; German.
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20-DEC-2001; 2001WO-EP015179.
                                 03-JAN-2001; 2001DE-01000127
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin isorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BST) of the invention
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
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                  Disclosure; Page 174; 1345pp; German.
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Matches 9; Conservative
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RESULT 695

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically senceded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                      Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
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                                                              ABV63285 standard; cDNA; 11 BP.
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                                                                                                                                                                                                Human skin EST 1071.
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Best Local Similarity
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                                                                                                                                                      21-OCT-2002
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                                            ABV63285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; cosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                         Length 11;
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                                                                Sequence 11 BP; 3 A; 4 C; 1 G; 3 T; 0 U; 0 Other
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                                                                                                                                                                                                                                                                                                                                               ABV71904 standard; cDNA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                              13 CCCTTCCTAAG 23
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriatis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                                         M, Hofmann K;
                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 68; 1345pp; German.
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                                                                                                                         20-DEC-2001; 2001WO-EP015179.
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                           WO200253774-A2.
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                                Homo sapiens
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (MI) is useful for identify skin-expressed genes and quantify their expression determine skin homeostasis, and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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Pred. No. 3.2e+02;
0; Mismatches 2; Indels
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                                                                                                                                           Disclosure; Page 102; 1345pp; German.
               Hofmann K;
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Best Local Similarity 81.00,
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               Conradt M,
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                                             WPI; 2002-590638/63.
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               Petersohn D,
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Sequence 11 BP; 3 A; 7 C; 0 G; 1 T; 0 U; 0 Other;

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Gaps
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 Score 7.8; DB 1; Length 11;
Pred. No. 3.2e+02;
0; Mismatches 2; Indels
30.0%;
81.8%;
                    9; Conservative
                                         12 CCCCTTCCTAA 22
                                                    Query Match
Best Local Similarity
                    Matches
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ABV68556 standard; cDNA; 11 BP. (first entry) Human skin EST 6342 21-OCT-2002 ABV68556; **ABV68556**, RESULT

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2

11-JUL-2002

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127.

(HENK) HENKEL KGAA

Conradt M, Petersohn D,

Hofmann K;

WPI; 2002-590638/63

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 201; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; sosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Sequence 11 BP; 3 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

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Score 7.8; DB 1; Length 11; Pred. No. 3.2e+02; 0; Mismatches 2; Indels
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosaces; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                            Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

ö The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

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               ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (BST) of the invention
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20-DEC-2001; 2001WO-EP015179
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(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaeis, scleroderma; ichthyosis; atopic dermatitis; acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                     Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytostatic; SAGB; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 BP; 3 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
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                                                                                 ABV66854 standard; cDNA; 11 BP.
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                          Human skin EST 4640.
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                                                                   ABV66854,
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosaces, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Best Local Similarity 81.8%,
9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. skin cancer.
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                                                                                                                                      Homo sapiens
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                                                                                      In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                   Disclosure; Page 205; 1345pp; German.
                                            Hofmann K;
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03-JAN-2001; 2001DE-01000127.
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9; Conservative
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                                           Conradt M,
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                    (HENK ) HENKEL KGAA
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Matches 9; Conserv
                                                                                                              e.g. skin cancer.
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Disclosure; Page 92; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expression in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhes; lupus erythematosus; ichthyosis; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

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Best Local Similarity 81.00,
Best Local 9; Conservative 21-OCT-2002 (first entry) 5 CTCATCGCCCC 15 1 crcaacccccc 11 skin. The present seque (EST) of the invention Human skin EST 5140. (HENK) HENKEL KGAA WPI; 2002-590638/63. WO200253774-A2 Petersohn D, Homo sapiens 11-JUL-2002. ABV67354; RESULT 711 ABV67354/c

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis, atopic dermatitis, acne, sebornhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                          Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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                ABV71549 standard; cDNA; 11 BP
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                                                                                                                                       Human skin EST 9335.
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09-APR-2002
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                                                        ABV71549;
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ABK28791
ABV71549/c
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(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, soleroderma; ichthyosis, atopic dermatitis; acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGB; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                            Gaps
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                                                Score 7.8; DB 1; Length 11;
Pred. No. 3.2e+02;
); Mismatches 2; Indels
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          Sequence 11 BP; 4 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; Page 288; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hofmann
                                                                                                                                                                                                                                                                       ABV71192 standard; cDNA; 11 BP.
                                              h 30.0%;
Similarity 81.8%;
9; Conservative (
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                                                                                                                                                                                                                                                                                                                                                     21-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                6 TCATCGCCCCT 16
                                                                                                                                                   11 TCCTCTCCCCT 1
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                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                               ABV71192;
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HSV-1; HSV-2; HPV; HBV; ss; probe; microorganism classification; infectious disease; genetic abnormality; cancer; capture sequence; blocker probe.

Query Match Best Loc Matches

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RESULT 713

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Gaps

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AAK99270;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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AAK99270
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                                                                                                                                                                                                                                                                                                               The invention relates to detecting a target nucleic acid comprising (a) hybridising a single-stranded or partially single-stranded target nucleic acid, to a capture sequence probe and a signal sequence probe to form double-stranded hybridish between the probes and the target nucleic acid, where the capture sequence probe and the signal sequence probe are capable of hybridishing to non-overlapping regions within the target nucleic acid and not hybridishing to each other. (b) adding a blocker probe to the hybridisation reaction, where the blocker probe hybridises capture sequence probes, (c) hinding the hybrid to excess non-hybridised capture sequence probes, (c) hinding the hybrid to a solid phase to form a bound hybrid, and (d) detecting the bound hybrid. The method is used to detecting a target nucleic acid. The method is used classifying microorganisms, diagnosing infectious diseases, detecting and characterising genetic abnormalities, identifying and classifying microorganisms, diagnosing infectious diseases, and measuring response to various types of treatment. The method is also useful for detecting the presence of nucleic acid in test samples. The method is not only rapid and sensitive, but is also highly specific and capable of discriminating highly homologous nucleic acid target sequences. Blocker probes are used in the method to eliminate excess capture sequence probes are used in the present sequence is a blocker probe derived from HSV-1, HSV-2, HPV or HBV sequences. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                        Detecting a target nucleic acid, for identifying microorganisms, diagnosing infections or detecting genetic abnormalities, comprises producing and detecting double-stranded hybrids between probes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                          Tang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                         Troy J,
                                                                                                                                                                      Williams I,
                                                                                                                                                                                                                                                                                            Claim 53; Page 21; 128pp; English.
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ID AAD46205 standard; DNA; 11 BP.
                                                                                          15-JUN-2001; 2001WO-US019353
                                                                                                                 15-JUN-2000; 2000US-00594839
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1es 9; Conservative
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           Human herpesvirus 1.
                                                                                                                                                                                                  WPI; 2002-130748/17.
                                                                                                                                                                                                                                                                   target nucleic acid.
                                                                                                                                             (DIGE-) DIGENE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cloning vector; ss
                                  WO200196608-A1
                                                                                                                                                                       Anthony J,
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Matches
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The invention relates to bacteriophage or a plasmid cloning vector which comprises a construction segment and a replaceable segment or a bacterial artificial chromosome (pBAC) or its segment comprising at least an origin of replication (ori). The invention also relates to methods for molecular cloning. The bacteriophage or plasmid cloning vectors are useful for in vivo or in vivo method of cloning nucleic acid inserts of interest used as tools in molecular genetic research. The present sequence is a linker oligonucleotide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New bacteriophage or plasmid cloning vectors, useful for in vitro or in vivo cloning nucleic acid inserts of interest used as tools in molecular genetic research.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.0%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 3.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 52; 162pp; English.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                  (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y,
                                                              WO200270720-A1.
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Unidentified.
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